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(54) Title: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES THEREFOR

(57) Abstract: The present invention provides the enzyme and enzymatic procedures for cleaving the β secretase cleavage site off the APP protein and associated nucleic acids, peptides, vectors, cells and cell isolates and assays. The invention further provides a modified APP protein and associated nucleic acids, peptides, vectors, cells, and cell isolates, and assays that are particularly useful for identifying candidate therapeutics for treatment or prevention of Alzheimer's disease.

Alzheimer's Disease Secretase, APP Substrates Therefor, and Uses Therefor

The present application is a continuation of United States Application Serial No. 09/416,901, filed October 13, 1999 which claims priority benefit of United States Provisional Patent Application No. 60/155,493, filed September 23, 1999. The present application also claims priority benefit as a continuation-in-part of United States Patent Application Serial No. 09/404,133 and PCT/US99/20881, both filed September 23, 1999, both of which in turn claim priority benefit of United States Provisional Patent Application No. 60/101,594, filed September 24, 1998. All of 10 these priority applications are hereby incorporated by reference in their entirety.

FIELD OF THE INVENTION

The present invention relates to Alzheimer's Disease, amyloid protein precursor, amyloid beta peptide, and human aspartyl proteases, as well as a method for 15 the identification of agents that modulate the activity of these polypeptides and thereby are candidates to modulate the progression of Alzheimer's disease.

BACKGROUND OF THE INVENTION

Alzheimer's disease (AD) causes progressive dementia with consequent 20 formation of amyloid plaques, neurofibrillary tangles, gliosis and neuronal loss. The disease occurs in both genetic and sporadic forms whose clinical course and pathological features are quite similar. Three genes have been discovered to date which, when mutated, cause an autosomal dominant form of Alzheimer's disease. These encode the amyloid protein precursor (APP) and two related proteins, 25 presenilin-1 (PS1) and presenilin-2 (PS2), which, as their names suggest, are structurally and functionally related. Mutations in any of the three proteins have been observed to enhance proteolytic processing of APP via an intracellular pathway that produces amyloid beta peptide (A β peptide ,or sometimes here as Abeta), a 40-42 amino acid long peptide that is the primary component of amyloid plaque in AD.

Dysregulation of intracellular pathways for proteolytic processing may be central to the pathophysiology of AD. In the case of plaque formation, mutations in APP, PS1 or PS2 consistently alter the proteolytic processing of APP so as to enhance formation of A β 1-42, a form of the A β peptide which seems to be particularly amyloidogenic, and thus very important in AD. Different forms of APP range in size from 695-770 amino acids, localize to the cell surface, and have a single C-terminal transmembrane domain. Examples of specific isoforms of APP which are currently known to exist in humans are the 695-amino acid polypeptide described by Kang *et al.* (1987), *Nature* 325: 733-736 which is designated as the "normal" APP; the 751 amino acid polypeptide described by Ponte *et al.* (1988), *Nature* 331: 525-527 (1988) and Tanzi *et al.* (1988), *Nature* 331: 528-530; and the 770 amino acid polypeptide described by Kitaguchi *et. al.* (1988), *Nature* 331: 530-532. The Abeta peptide is derived from a region of APP adjacent to and containing a portion of the transmembrane domain. Normally, processing of APP at the α -secretase site cleaves the midregion of the A β sequence adjacent to the membrane and releases the soluble, extracellular domain of APP from the cell surface. This α -secretase APP processing creates soluble APP- α , which is normal and not thought to contribute to AD. Pathological processing of APP at the β - and γ -secretase sites, which are located N-terminal and C-terminal to the α -secretase site, respectively, produces a very different result than processing at the α site. Sequential processing at the β - and γ -secretase sites releases the A β peptide, a peptide possibly very important in AD pathogenesis. Processing at the β - and γ -secretase sites can occur in both the endoplasmic reticulum (in neurons) and in the endosomal/lysosomal pathway after reinternalization of cell surface APP (in all cells). Despite intense efforts, for 10 years or more, to identify the enzymes responsible for processing APP at the β and γ sites, to produce the A β peptide, those proteases remained unknown until this disclosure.

SUMMARY OF THE INVENTION

Here, for the first time, we report the identification and characterization of the 30 β secretase enzyme, termed Aspartyl Protease 2 (Asp2). We disclose some known

and some novel human aspartic proteases that can act as β -secretase proteases and, for the first time, we explain the role these proteases have in AD. We describe regions in the proteases critical for their unique function and for the first time characterize their substrate. This is the first description of expressed isolated purified active protein of
5 this type, assays that use the protein, in addition to the identification and creation of useful cell lines and inhibitors.

Here we disclose a number of variants of the Asp2 gene and peptide.

In one aspect, the invention provides any isolated or purified nucleic acid polynucleotide that codes for a protease capable of cleaving the beta (β) secretase cleavage site of APP that contains two or more sets of special nucleic acids, where
10 the special nucleic acids are separated by nucleic acids that code for about 100 to 300 amino acid positions, where the amino acids in those positions may be any amino acids, where the first set of special nucleic acids consists of the nucleic acids that code for the peptide DTG, where the first nucleic acid of the first special set of nucleic acids is the first special nucleic acid, and where the second set of nucleic acids code
15 for either the peptide DSG or DTG, where the last nucleic acid of the second set of nucleic acids is the last special nucleic acid, with the proviso that the nucleic acids disclosed in SEQ ID NO. 1 and SEQ ID NO. 3 are not included. In a preferred embodiment, the two sets of special nucleic acids are separated by nucleic acids that code for about 125 to 222 amino acid positions, which may be any amino acids. In a highly preferred embodiment, the two sets of special nucleic acids are separated by nucleic acids that code for about 150 to 196, or 150-190, or 150 to 172 amino acid positions, which may be any amino acids. In a particular preferred embodiment, the two sets are separated by nucleic acids that code for about 172 amino acid positions,
20 which may be any amino acids. An exemplary nucleic acid polynucleotide comprises the acid nucleotide sequence in SEQ ID NO. 5. In another particular preferred embodiment, the two sets are separated by nucleic acids that code for about 196 amino acids. An exemplary polynucleotide comprises the nucleotide sequence in SEQ ID NO. 5. In another particular embodiment, the two sets of nucleotides are separated by nucleic acids that code for about 190 amino acids. An exemplary polynucleotide
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comprises the nucleotide sequence in SEQ ID NO. 1. Preferably, the first nucleic acid of the first special set of amino acids, that is, the first special nucleic acid, is operably linked to any codon where the nucleic acids of that codon codes for any peptide comprising from 1 to 10,000 amino acid (positions). In one variation, the first special nucleic acid is operably linked to nucleic acid polymers that code for any peptide selected from the group consisting of: any reporter proteins or proteins which facilitate purification. For example, the first special nucleic acid is operably linked to nucleic acid polymers that code for any peptide selected from the group consisting of: immunoglobulin-heavy chain, maltose binding protein, glutathione S transferase, Green Fluorescent protein, and ubiquitin. In another variation, the last nucleic acid of the second set of special amino acids, that is, the last special nucleic acid, is operably linked to nucleic acid polymers that code for any peptide comprising any amino acids from 1 to 10,000 amino acids. In still another variation, the last special nucleic acid is operably linked to nucleic acid polymers that code for any peptide selected from the group consisting of: any reporter proteins or proteins which facilitate purification. For example, the last special nucleic acid is operably linked to nucleic acid polymers that code for any peptide selected from the group consisting of: immunoglobulin-heavy chain, maltose binding protein, glutathione S transferase, Green Fluorescent protein, and ubiquitin.

In a related aspect, the invention provides any isolated or purified nucleic acid polynucleotide that codes for a protease capable of cleaving the beta secretase cleavage site of APP that contains two or more sets of special nucleic acids, where the special nucleic acids are separated by nucleic acids that code for about 100 to 300 amino acid positions, where the amino acids in those positions may be any amino acids, where the first set of special nucleic acids consists of the nucleic acids that code for DTG, where the first nucleic acid of the first special set of nucleic acids is the first special nucleic acid, and where the second set of nucleic acids code for either DSG or DTG, where the last nucleic acid of the second set of special nucleic acids is the last special nucleic acid, where the first special nucleic acid is operably linked to nucleic acids that code for any number of amino acids from zero to 81 amino acids and where

each of those codons may code for any amino acid. In a preferred embodiment, the first special nucleic acid is operably linked to nucleic acids that code for any number of from 64 to 77 amino acids where each codon may code for any amino acid. In a particular embodiment, the first special nucleic acid is operably linked to nucleic acids
5 that code for 71 amino acids. For example, the first special nucleic acid is operably linked to 71 amino acids and where the first of those 71 amino acids is the amino acid T. In a preferred embodiment, the polynucleotide comprises a sequence that is at least 95% identical to a human Asp1 or Asp2 sequence as taught herein. In another preferred embodiment, the first special nucleic acid is operably linked to nucleic acids
10 that code for any number of from 30 to 54 amino acids, or 35 to 47 amino acids, or 40 to 54 amino acids where each codon may code for any amino acid. In a particular embodiment, the first special nucleic acid is operably linked to nucleic acids that code for 47 amino acids. For example, the first special nucleic acid is operably linked to 47 codons where the first those 47 amino acids is the amino acid E.

15 In another related aspect, the invention provides for any isolated or purified nucleic acid polynucleotide that codes for a protease capable of cleaving the beta (β) secretase cleavage site of APP and that contains two or more sets of special nucleic acids, where the special nucleic acids are separated by nucleic acids that code for about 100 to 300 amino acid positions, where the amino acids in those positions may
20 be any amino acids, where the first set of special nucleic acids consists of the nucleic acids that code for the peptide DTG, where the first nucleic acid of the first special set of amino acids is, the first special nucleic acid, and where the second set of special nucleic acids code for either the peptide DSG or DTG, where the last nucleic acid of the second set of special nucleic acids, the last special nucleic acid, is operably linked
25 to nucleic acids that code for any number of codons from 50 to 170 codons. In a preferred embodiment, the last special nucleic acid is operably linked to nucleic acids comprising from 100 to 170 codons. In a highly preferred embodiment, the last special nucleic acid is operably linked to nucleic acids comprising from 142 to 163 codons. In a particular embodiment, the last special nucleic acid is operably linked to
30 nucleic acids comprising about 142 codons, or about 163 codons, or about 170

codons. In a highly preferred embodiment, the polynucleotide comprises a sequence that is at least 95% identical to aspartyl-protease encoding sequences taught herein. In one variation, the second set of special nucleic acids code for the peptide DSG. In another variation, the first set of nucleic acid polynucleotide is operably linked to a 5 peptide purification tag. For example, the nucleic acid polynucleotide is operably linked to a peptide purification tag which is six histidine. In still another variation, the first set of special nucleic acids are on one polynucleotide and the second set of special nucleic acids are on a second polynucleotide, where both first and second polynucleotides have at least 50 codons. In one embodiment of this type, both of the 10 polynucleotides are in the same solution. In a related aspect, the invention provides a vector which contains a polynucleotide as described above, or a cell or cell line which is transformed or transfected with a polynucleotide as described above or with a vector containing such a polynucleotide.

In still another aspect, the invention provides an isolated or purified peptide or 15 protein comprising an amino acid polymer that is a protease capable of cleaving the beta (β) secretase cleavage site of APP that contains two or more sets of special amino acids, where the special amino acids are separated by about 100 to 300 amino acid positions, where each amino acid position can be any amino acid, where the first set of special amino acids consists of the peptide DTG, where the first amino acid of the 20 first special set of amino acids is, the first special amino acid, where the second set of amino acids is selected from the peptide comprising either DSG or DTG, where the last amino acid of the second set of special amino acids is the last special amino acid, with the proviso that the proteases disclosed in SEQ ID NO. 2 and SEQ ID NO. 4 are not included. In preferred embodiments, the two sets of amino acids are separated by 25 about 125 to 222 amino acid positions or about 150 to 196 amino acids, or about 150-190 amino acids, or about 150 to 172 amino acids, where in each position it may be any amino acid. In a particular embodiment, the two sets of amino acids are separated by about 172 amino acids. For example, the protease has the amino acid sequence described in SEQ ID NO 6. In another particular embodiment, the two sets of amino 30 acids are separated by about 196 amino acids. For example, the two sets of amino

acids are separated by the same amino acid sequences that separate the same set of special amino acids in SEQ ID NO 4. In another particular embodiment, the two sets of nucleotides are separated by about 190 amino acids. For example, the two sets of nucleotides are separated by the same amino acid sequences that separate the same set of special amino acids in SEQ ID NO 2. In one embodiment, the first amino acid of the first special set of amino acids, that is, the first special amino acid, is operably linked to any peptide comprising from 1 to 10,000 amino acids. In another embodiment, the first special amino acid is operably linked to any peptide selected from the group consisting of: any reporter proteins or proteins which facilitate purification. In particular embodiments, the first special amino acid is operably linked to any peptide selected from the group consisting of: immunoglobulin-heavy chain, maltose binding protein, glutathione S transferase, Green Fluorescent protein, and ubiquitin. In still another variation, the last amino acid of the second set of special amino acids, that is, the last special amino acid, is operably linked to any peptide comprising any amino acids from 1 to 10,000 amino acids. By way of nonlimiting example, the last special amino acid is operably linked any peptide selected from the group consisting of any reporter proteins or proteins which facilitate purification. In particular embodiments, the last special amino acid is operably linked to any peptide selected from the group consisting of: immunoglobulin-heavy chain, maltose binding protein, glutathione S transferase, Green Fluorescent protein, and ubiquitin.

In a related aspect, the invention provides any isolated or purified peptide or protein comprising an amino acid polypeptide that codes for a protease capable of cleaving the beta secretase cleavage site of APP that contains two or more sets of special amino acids, where the special amino acids are separated by about 100 to 300 amino acid positions, where each amino acid in each position can be any amino acid, where the first set of special amino acids consists of the amino acids DTG, where the first amino acid of the first special set of amino acids is, the first special amino acid, D, and where the second set of amino acids is either DSG or DTG, where the last amino acid of the second set of special amino acids is the last special amino acid, G, where the first special amino acid is operably linked to amino acids that code for any

number of amino acids from zero to 81 amino acid positions where in each position it may be any amino acid. In a preferred embodiment, the first special amino acid is operably linked to a peptide from about 30-77 or about 64 to 77 amino acids positions where each amino acid position may be any amino acid. In a particular embodiment, 5 the first special amino acid is operably linked to a peptide 35, 47, 71, or 77 amino acids. In a very particular embodiment, the first special amino acid is operably linked to 71 amino acids and the first of those 71 amino acids is the amino acid T. For example, the polypeptide comprises a sequence that is at least 95% identical to an aspartyl protease sequence as described herein. In another embodiment, the first 10 special amino acid is operably linked to any number of from 40 to 54 amino acids (positions) where each amino acid position may be any amino acid. In a particular embodiment, the first special amino acid is operably linked to amino acids that code for a peptide of 47 amino acids. In a very particular embodiment, the first special amino acid is operably linked to a 47 amino acid peptide where the first those 47 15 amino acids is the amino acid E. In another particular embodiment, the first special amino acid is operably linked to the same corresponding peptides from SEQ ID NO. 3 that are 35, 47, 71, or 77 peptides in length, beginning counting with the amino acids on the first special sequence, DTG, towards the N-terminal of SEQ ID NO. 3. In another particular embodiment, the polypeptide comprises a sequence that is at least 20 95% identical to the same corresponding amino acids in SEQ ID NO. 4, that is, identical to that portion of the sequences in SEQ ID NO. 4, including all the sequences from both the first and or the second special nucleic acids, toward the - terminal, through and including 71, 47, 35 amino acids before the first special amino acids. For example, the complete polypeptide comprises the peptide of 71 amino 25 acids, where the first of the amino acid is T and the second is Q.

In still another related aspect, the invention provides any isolated or purified amino acid polypeptide that is a protease capable of cleaving the beta (β) secretase cleavage site of APP that contains two or more sets of special amino acids, where the special amino acids are separated by about 100 to 300 amino acid positions, where 30 each amino acid in each position can be any amino acid, where the first set of special

amino acids consists of the amino acids that code for DTG, where the first amino acid of the first special set of amino acids is, the first special amino acid, D, and where the second set of amino acids are either DSG or DTG, where the last amino acid of the second set of special amino acids is the last special amino acid, G, which is operably linked to any number of amino acids from 50 to 170 amino acids, which may be any amino acids. In preferred embodiments, the last special amino acid is operably linked to a peptide of about 100 to 170 amino acids or about 142-163 amino acids. In particular embodiments, the last special amino acid is operably linked to a peptide of about 142 amino acids, or about 163 amino acids, or about 170 amino acids. For example, the polypeptide comprises a sequence that is at least 95% identical (and preferably 100% identical) to an aspartyl protease sequence as described herein. In one particular embodiment, the second set of special amino acids is comprised of the peptide with the amino acid sequence DSG. Optionally, the amino acid polypeptide is operably linked to a peptide purification tag, such as purification tag which is six histidine. In one variation, the first set of special amino acids are on one polypeptide and the second set of special amino acids are on a second polypeptide, where both first and second polypeptide have at least 50 amino acids, which may be any amino acids. In one embodiment of this type, both of the polypeptides are in the same vessel. The invention further includes a process of making any of the polynucleotides, vectors, or cells described herein; and a process of making any of the polypeptides described herein.

In yet another related aspect, the invention provides a purified polynucleotide comprising a nucleotide sequence that encodes a polypeptide having aspartyl protease activity, wherein the polypeptide has an amino acid sequence characterized by: (a) a first tripeptide sequence DTG; (b) a second tripeptide sequence selected from the group consisting of DSG and DTG; and (c) about 100 to 300 amino acids separating the first and second tripeptide sequences, wherein the polypeptide cleaves the beta secretase cleavage site of amyloid protein precursor. In one embodiment, the polypeptide comprises an amino acid sequence depicted in SEQ ID NO: 2 or 4, whereas in another embodiment, the polypeptide comprises an amino acid sequence

other than the amino acid sequences set forth in SEQ ID NOs: 2 and 4. Similarly, the invention provides a purified polynucleotide comprising a nucleotide sequence that encodes a polypeptide that cleaves the beta secretase cleavage site of amyloid protein precursor; wherein the polynucleotide includes a strand that hybridizes to one or more 5 of SEQ ID NOs: 3, 5, and 7 under the following hybridization conditions:
hybridization overnight at 42°C for 2.5 hours in 6 X SSC/0.1% SDS, followed by washing in 1.0 X SSC at 65°C, 0.1% SDS. In one embodiment, the polypeptide comprises an amino acid sequence depicted in SEQ ID NO: 2 or 4, whereas in another embodiment, the polypeptide comprises an amino acid sequence other than the amino 10 acid sequences set forth in SEQ ID NOs: 2 and 4. Likewise, the invention provides a purified polypeptide having aspartyl protease activity, wherein the polypeptide is encoded by polynucleotides as described in the preceding sentences. The invention also provides a vector or host cell comprising such polynucleotides, and a method of making the polypeptides using the vectors or host cells to recombinantly express the 15 polypeptide.

In yet another aspect, the invention provides an isolated nucleic acid molecule comprising a polynucleotide, said polynucleotide encoding a Hu-Asp polypeptide and having a nucleotide sequence at least 95% identical to a sequence selected from the group consisting of:

20 (a) a nucleotide sequence encoding a Hu-Asp polypeptide selected from the group consisting of Hu-Asp1, Hu-Asp2(a), and Hu-Asp2(b), wherein said Hu-Asp1, Hu-Asp2(a) and Hu-Asp2(b) polypeptides have the complete amino acid sequence of SEQ ID NO. 2, SEQ ID NO. 4, and SEQ ID NO. 6, respectively; and
25 (b) a nucleotide sequence complementary to the nucleotide sequence of (a).

Several species are particularly contemplated. For example, the invention provides a nucleic acid and molecule wherein said Hu-Asp polypeptide is Hu-Asp1, and said polynucleotide molecule of 1(a) comprises the nucleotide sequence of SEQ ID NO. 1; and a nucleic acid molecule wherein said Hu-Asp polypeptide is 30 Hu-Asp2(a), and said polynucleotide molecule of 1(a) comprises the nucleotide

sequence of SEQ ID NO. 4; and a nucleic acid molecule wherein said Hu-Asp polypeptide is Hu-Asp2(b), and said polynucleotide molecule of 1(a) comprises the nucleotide sequence of SEQ ID NO. 5. In addition to the foregoing, the invention provides an isolated nucleic acid molecule comprising polynucleotide which
5 hybridizes under stringent conditions to a polynucleotide having the nucleotide sequence in (a) or (b) as described above.

Additionally, the invention provides a vector comprising a nucleic acid molecule as described in the preceding paragraph. In a preferred embodiment, the nucleic acid molecule is operably linked to a promoter for the expression of a Hu-Asp
10 polypeptide. Individual vectors which encode Hu-Asp1, and Hu-Asp2(a), and Hu-Asp2(b) are all contemplated. Likewise, the invention contemplates a host cell comprising any of the foregoing vectors, as well as a method of obtaining a Hu-Asp polypeptide comprising culturing such a host cell and isolating the Hu-Asp polypeptide. Host cells of the invention include bacterial cells, such as *E. coli*, and
15 eukaryotic cells. Among the eukaryotic cells that are contemplated are insect cells, such as sf9 or High 5 cells; and mammalian cells, such as human, rodent, lagomorph, and primate. Preferred human cells include HEK293, and IMR-32 cells. Other preferred mammalian cells include COS-7, CHO-K1, Neuro-2A, and 3T3 cells. Also among the eukaryotic cells that are contemplated are a yeast cell and an avian cell.

20 In a related aspect, the invention provides an isolated Hu-Asp1 polypeptide comprising an amino acid sequence at least 95% identical to a sequence comprising the amino acid sequence of SEQ ID NO. 2. The invention also provides an isolated Hu-Asp2(a) polypeptide comprising an amino acid sequence at least 95% identical to a sequence comprising the amino acid sequence of SEQ ID NO. 4. The invention also
25 provides an isolated Hu-Asp2(a) polypeptide comprising an amino acid sequence at least 95% identical to a sequence comprising the amino acid sequence of SEQ ID NO.
8.

In still another aspect, the invention provides an isolated antibody that binds specifically to any Hu-Asp polypeptide described herein, especially the polypeptide
30 described in the preceding paragraphs.

The invention also provides several assays involving aspartyl protease enzymes of the invention. For example, the invention provides

a method to identify a cell that can be used to screen for inhibitors of β secretase activity comprising:

5 (a) identifying a cell that expresses a protease capable of cleaving APP at the β secretase site, comprising:

i) collect the cells or the supernatant from the cells to be identified

10 ii) measure the production of a critical peptide, where the critical peptide is selected from the group consisting of either the APP C-terminal peptide or soluble APP,

iii) select the cells which produce the critical peptide.

In one variation, the cells are collected and the critical peptide is the APP C-terminal peptide created as a result of the β secretase cleavage. In another variation, the supernatant is collected and the critical peptide is soluble APP, where the soluble APP has a C-terminus created by β secretase cleavage. In preferred embodiments, the cells contain any of the nucleic acids or polypeptides described above and the cells are shown to cleave the β secretase site of any peptide having the following peptide structure, P2, P1, P1', P2', where P2 is K or N, where P1 is M or L, where P1' is D, where P2' is A. The method of claim 111 where P2 is K and P1 is M. The method of claim 112 where P2 is N and P1 is L.

In still another aspect, the invention provides novel isoforms of amyloid protein precursor (APP) where the last two carboxy terminus amino acids of that isoform are both lysine residues. In this context, the term "isoform" is defined as any APP polypeptide, including APP variants (including mutations), and APP fragments that exists in humans, such as those described in US 5,766,846, col 7, lines 45-67, incorporated into this document by reference, modified as described herein by the inclusion of two C-terminal lysine residues. For example, the invention provides a polypeptide comprising the isoform known as APP695, modified to include two lysine residues as its last two carboxy terminus amino acids. An exemplary polypeptide

comprises the amino acid sequence set forth in SEQ ID NO. 16. The invention further includes APP isoform variants as set forth in SEQ ID NOS. 18 and 20. The invention further includes all polynucleotides that encode an APP protein that has been modified to include two C-terminal lysines; as well has any eukaryotic cell line comprising such nucleic acids or polypeptides. Preferred cell lines include a mammalian cell line (*e.g.*, HEK293, Neuro2a).

Thus, in one embodiment, the invention provides a polypeptide comprising the amino acid sequence of a mammalian amyloid protein precursor (APP) or fragment thereof containing an APP cleavage site recognizable by a mammalian β -secretase, and further comprising two lysine residues at the carboxyl terminus of the amino acid sequence of the mammalian APP or APP fragment. As taught herein in detail, the addition of two additional lysine residues to APP sequences has been found to greatly increase A β processing of the APP in APP processing assays. Thus, the di-lysine modified APP reagents of the invention are particularly useful in assays to identify modulators of A β production, for use in designing therapeutics for the treatment or prevention of Alzheimer's disease. In one embodiment, the polypeptide comprises the complete amino acid sequence of a mammalian amyloid protein precursor (APP), and further comprises the two lysine residues at the carboxyl terminus of the amino acid sequence of the mammalian amyloid protein precursor. In an alternative embodiment, the polypeptide comprises only a fragment of the APP, the fragment containing at least that portion of APP that is cleaved by a mammalian β -secretase in the formation of A β peptides.

The practice of assays that monitor cleavage of APP can be facilitated by attaching a marker to a portion of the APP. Measurement of retained or liberated marker can be used to quantitate the amount of APP cleavage that occurs in the assay, *e.g.*, in the presence or absence of a putative modulator of cleavage activity. Thus, in one preferred embodiment, the polypeptide of the invention further includes a marker. For example, the marker comprises a reporter protein amino acid sequence attached to the APP amino acid sequence. Exemplary reporter proteins include a fluorescing protein (*e.g.*, green fluorescing proteins, luciferase) or an enzyme that is used to

cleave a substrate to produce a colorimetric cleavage product. Also contemplated are tag sequences which are commonly used as epitopes for quantitative immunoassays.

In a preferred embodiment, the di-lysine-modified APP of the invention is a human APP. For example, human APP isoforms such as APP695, APP751, and APP770, modified to include the two lysines, are contemplated. In a preferred embodiment, the APP isoform comprises at least one variation selected from the group consisting of a Swedish KM-NL mutation and a London V717-F mutation, or any other mutation that has been observed in a subpopulation that is particularly prone to development of Alzheimer's disease. These mutations are recognized as mutations that influence APP processing into A β . In a highly preferred embodiment, the APP protein or fragment thereof comprises the APP-Sw β -secretase peptide sequence NLDA (SEQ ID NO: 66), which is associated with increased levels of A β processing and therefore is particularly useful in assays relating to Alzheimer's research. More particularly, the APP protein or fragment thereof preferably comprises the APP-Sw β -secretase peptide sequence SEVNLDAEFR (SEQ ID NO: 63).

In one preferred embodiment, the APP protein or fragment thereof further includes an APP transmembrane domain carboxy-terminal to the APP-Sw β -secretase peptide sequence. Polypeptides that include the TM domain are particularly useful in cell-based APP processing assays. In contrast, embodiments lacking the TM domain are useful in cell-free assays of APP processing.

In addition to working with APP from humans and various animal models, researchers in the field of Alzheimer's also have construct chimeric APP polypeptides which include stretches of amino acids from APP of one species (e.g., humans) fused to stretches of APP from one or more other species (e.g., rodent). Thus, in another embodiment of the polypeptide of the invention, the APP protein or fragment thereof comprises a chimeric APP, the chimeric APP including partial APP amino acid sequences from at least two species. A chimeric APP that includes amino acid sequence of a human APP and a rodent APP is particularly contemplated.

In a related aspect, the invention provides a polynucleotide comprising a nucleotide sequence that encodes a polypeptide as described in the preceding

paragraphs. Such a polynucleotide is useful for recombinant expression of the polypeptide of the invention for use in APP processing assays. In addition, the polynucleotide is useful for transforming into cells to produce recombinant cells that express the polypeptide of the invention, which cells are useful in cell-based assays to identify modulators of APP processing. Thus, in addition to polynucleotides, the invention provides a vector comprising such polynucleotides, especially expression vectors where the polynucleotide is operably linked to a promoter to promote expression of the polypeptide encoded by the polynucleotide in a host cell. The invention further provides a host cell transformed or transfected with a polynucleotide according to claim 14 or a vector according to claim 15 or 16. Among the preferred host cells are mammalian cells, especially human cells.

In another, related embodiment, the invention provides a polypeptide useful for assaying for modulators of β -secretase activity, said polypeptide comprising an amino acid sequence of the formula $\text{NH}_2\text{-X-Y-Z-KK-COOH}$; wherein X, Y, and Z each comprise an amino acid sequence of at least one amino acid; wherein $\text{-NH}_2\text{-X}$ comprises an amino-terminal amino acid sequence having at least one amino acid residue; wherein Y comprises an amino acid sequence of a β -secretase recognition site of a mammalian amyloid protein precursor (APP); and wherein Z-KK-COOH comprises a carboxy-terminal amino acid sequence ending in two lysine (K) residues.

In one preferred variation, the carboxyl-terminal amino acid sequence Z includes a hydrophobic domain that is a transmembrane domain in host cells that express the polypeptide. Host cells that express such a polypeptide are particularly useful in assays described herein for identifying modulators of APP processing. In another preferred variation, the amino-terminal amino acid sequence X includes an amino acid sequence of a reporter or marker protein, as described above. In still another preferred variation, the β -secretase recognition site Y comprises the human APP-Sw β -secretase peptide sequence NLDA (SEQ ID NO: 66). It will be apparent that these preferred variations are not mutually exclusive of each other -- they may be combined in a single polypeptide. The invention further provides a polynucleotide comprising a nucleotide sequence that encodes such polypeptides, vectors which comprise such

polynucleotides, and host cells which comprises such vectors, polynucleotides, and/or polypeptides.

In yet another aspect, the invention provides a method for identifying inhibitors of an enzyme that cleaves the beta secretase cleavable site of APP comprising:

- 5 a) culturing cells in a culture medium under conditions in which the enzyme causes processing of APP and release of amyloid beta-peptide into the medium and causes the accumulation of CTF99 fragments of APP in cell lysates,
- 10 b) exposing the cultured cells to a test compound; and specifically determining whether the test compound inhibits the function of the enzyme by measuring the amount of amyloid beta-peptide released into the medium and/or the amount of CTF99 fragments of APP in cell lysates;
- 15 c) identifying test compounds diminishing the amount of soluble amyloid beta peptide present in the culture medium and diminution of CTF99 fragments of APP in cell lysates as Asp2 inhibitors. In preferred embodiments, the cultured cells are a human, rodent or insect cell line. It is also preferred that the human or rodent cell line exhibits β secretase activity in which processing of APP occurs with release of amyloid beta-peptide into the culture medium and accumulation of CTF99 in cell lysates. Among the contemplated test compounds are antisense oligomers directed against the enzyme that exhibits β secretase activity, which oligomers reduce release of soluble amyloid beta-peptide into the culture medium and accumulation of CTF99 in cell lysates.
- 20 d) determining the amount of soluble amyloid beta-peptide present in the culture medium and diminution of CTF99 fragments of APP in cell lysates as Asp2 inhibitors. In preferred embodiments, the cultured cells are a human, rodent or insect cell line. It is also preferred that the human or rodent cell line exhibits β secretase activity in which processing of APP occurs with release of amyloid beta-peptide into the culture medium and accumulation of CTF99 in cell lysates. Among the contemplated test compounds are antisense oligomers directed against the enzyme that exhibits β secretase activity, which oligomers reduce release of soluble amyloid beta-peptide into the culture medium and accumulation of CTF99 in cell lysates.

In yet another aspect, the invention provides a method for the identification of an agent that decreases the activity of a Hu-Asp polypeptide selected from the group consisting of Hu-Asp1, Hu-Asp2(a), and Hu-Asp2(b), the method comprising:

- 25 a) determining the activity of said Hu-Asp polypeptide in the presence of a test agent and in the absence of a test agent; and
- 30 b) comparing the activity of said Hu-Asp polypeptide determined in the presence of said test agent to the activity of said Hu-Asp polypeptide determined in the absence of said test agent; whereby a lower level of activity in the presence of said

test agent than in the absence of said test agent indicates that said test agent has decreased the activity of said Hu-Asp polypeptide.

In a related aspect, the invention provides a method for assaying for modulators of β -secretase activity, comprising the steps of:

- 5 (a) contacting a first composition with a second composition both in the presence and in the absence of a putative modulator compound, wherein the first composition comprises a mammalian β -secretase polypeptide or biologically active fragment thereof, and wherein the second composition comprises a substrate polypeptide having an amino acid sequence comprising a β -secretase cleavage site;
- 10 (b) measuring cleavage of the substrate polypeptide in the presence and in the absence of the putative modulator compound; and (c) identifying modulators of β -secretase activity from a difference in cleavage in the presence versus in the absence of the putative modulator compound. A modulator that is a β -secretase antagonist (inhibitor) reduces such cleavage, whereas a modulator that is a β -secretase agonist increases such cleavage. Since such assays are relevant to development of
- 15 Alzheimer's disease therapeutics for humans, it will be readily apparent that, in one preferred embodiment, the first composition comprises a purified human Asp2 polypeptide. In one variation, the first composition comprises a soluble fragment of a human Asp2 polypeptide that retains Asp2 β -secretase activity. Several such fragments (including Δ TM fragments) are described herein in detail. Thus, in a particular embodiment, the soluble fragment is a fragment lacking an Asp2 transmembrane domain.
- 20

The β -secretase cleavage site in APP is known, and it will be appreciated that the assays of the invention can be performed with either intact APP or fragments or analogs of APP that retain the β -secretase recognition and cleavage site. Thus, in one variation, the substrate polypeptide of the second composition comprises the amino acid sequence SEVNLDAEFR (SEQ ID NO: 63), which includes the β -secretase recognition site of human APP that contains the "Swiss" mutation. In another variation, the substrate polypeptide of the second composition comprises the amino acid sequence EVKMDAEF (SEQ ID NO: 67). In another

variation, the second composition comprises a polypeptide having an amino acid sequence of a human amyloid precursor protein (APP). For example, the human amyloid precursor protein is selected from the group consisting of: APP695, APP751, and APP770. Preferably, the human amyloid precursor protein (irrespective of isoform selected) includes at least one mutation selected from a K-M-N-L Swiss mutation and a V-F London mutation. As explained elsewhere, one preferred embodiment involves a variation wherein the polypeptide having an amino acid sequence of a human APP further comprises an amino acid sequence comprising a marker sequence attached amino-terminal to the amino acid sequence of the human amyloid precursor protein. Preferably, the polypeptide having an amino acid sequence of a human APP further comprises two lysine residues attached to the carboxyl terminus of the amino acid sequence of the human APP. The assays can be performed in a cell free setting, using cell-free enzyme and cell-free substrate, or can be performed in a cell-based assay wherein the second composition comprises a eukaryotic cell that expresses amyloid precursor protein (APP) or a fragment thereof containing a β -secretase cleavage site. Preferably, the APP expressed by the host cell is an APP variant that includes two carboxyl-terminal lysine residues. It will also be appreciated that the β -secretase enzyme can be an enzyme that is expressed on the surface of the same cells.

The present invention provides isolated nucleic acid molecules comprising a polynucleotide that codes for a polypeptide selected from the group consisting of human aspartyl proteases. In particular, human aspartyl protease 1 (Hu-Asp1) and two alternative splice variants of human aspartyl protease-2 (Hu-Asp2), a "long" (L) form designated herein as Hu-Asp2(a) and a "short" (S) form designated Hu-Asp2(b). As used herein, all references to "Hu-Asp" should be understood to refer to all of Hu-Asp1, Hu-Asp2(a), and Hu-Asp2(b). In addition, as used herein, all references to "Hu-Asp2" should be understood to refer to both Hu-Asp2(a) and Hu-Asp2(b). Hu-Asp1 is expressed most abundantly in pancreas and prostate tissues, while Hu-Asp2(a) and Hu-Asp2(b) are expressed most abundantly in pancreas and brain

tissues. The invention also provides isolated Hu-Asp1, Hu-Asp2(a), and Hu-Asp2(b) polypeptides, as well as fragments thereof which exhibit aspartyl protease activity.

In a preferred embodiment, the nucleic acid molecules comprise a polynucleotide having a nucleotide sequence selected from the group consisting of residues 1-1554 of SEQ ID NO. 1, encoding Hu-Asp1, residues 1-1503 of SEQ ID NO. 3, encoding Hu-Asp2(a), and residues 1-1428 of SEQ ID NO. 5, encoding Hu-Asp2(b). In another aspect, the invention provides an isolated nucleic acid molecule comprising a polynucleotide which hybridizes under stringent conditions to a polynucleotide encoding Hu-Asp1, Hu-Asp2(a), Hu-Asp2(b), or fragments thereof. European patent application EP 0 848 062 discloses a polypeptide referred to as "Asp 1," that bears substantial homology to Hu-Asp1, while international application WO 98/22597 discloses a polypeptide referred to as "Asp 2," that bears substantial homology to Hu-Asp2(a).

The present invention also provides vectors comprising the isolated nucleic acid molecules of the invention, host cells into which such vectors have been introduced, and recombinant methods of obtaining a Hu-Asp1, Hu-Asp2(a), or Hu-Asp2(b) polypeptide comprising culturing the above-described host cell and isolating the relevant polypeptide.

In another aspect, the invention provides isolated Hu-Asp1, Hu-Asp2(a), and Hu-Asp2(b) polypeptides, as well as fragments thereof. In a preferred embodiment, the Hu-Asp1, Hu-Asp2(a), and Hu-Asp2(b) polypeptides have the amino acid sequence given in SEQ ID NO. 2, SEQ ID NO. 4, or SEQ ID NO. 6, respectively. The present invention also describes active forms of Hu-Asp2, methods for preparing such active forms, methods for preparing soluble forms, methods for measuring Hu-Asp2 activity, and substrates for Hu-Asp2 cleavage. The invention also describes antisense oligomers targeting the Hu-Asp1, Hu-Asp2(a) and Hu-Asp2(b) mRNA transcripts and the use of such antisense reagents to decrease such mRNA and consequently the production of the corresponding polypeptide. Isolated antibodies, both polyclonal and monoclonal, that binds specifically to any of the Hu-Asp1, Hu-Asp2(a), and Hu-Asp2(b) polypeptides of the invention are also provided.

The invention also provides a method for the identification of an agent that modulates the activity of any of Hu-Asp1, Hu-Asp2(a), and Hu-Asp2(b). The inventions

describes methods to test such agents in cell-free assays to which Hu-Asp2 polypeptide is added, as well as methods to test such agents in human or other mammalian cells in which Hu-Asp2 is present.

Additional features and variations of the invention will be apparent to
5 those skilled in the art from the entirety of this application, including the drawing and detailed description, and all such features are intended as aspects of the invention. Likewise, features of the invention described herein can be re-combined into additional embodiments that are also intended as aspects of the invention, irrespective of whether the combination of features is specifically mentioned above as an aspect or embodiment
10 of the invention. Also, only such limitations which are described herein as critical to the invention should be viewed as such; variations of the invention lacking limitations which have not been described herein as critical are intended as aspects of the invention.

In addition to the foregoing, the invention includes, as an additional aspect, all embodiments of the invention narrower in scope in any way than the variations
15 specifically mentioned above. Although the applicant(s) invented the full scope of the claims appended hereto, the claims appended hereto are not intended to encompass within their scope the prior art work of others. Therefore, in the event that statutory prior art within the scope of a claim is brought to the attention of the applicants by a Patent Office or other entity or individual, the applicant(s) reserve the right to exercise
20 amendment rights under applicable patent laws to redefine the subject matter of such a claim to specifically exclude such statutory prior art or obvious variations of statutory prior art from the scope of such a claim. Variations of the invention defined by such amended claims also are intended as aspects of the invention.

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BRIEF DESCRIPTION OF THE SEQUENCE LISTING

Sequence ID No. 1: Human Asp-1, nucleotide sequence.

Sequence ID No. 2: Human Asp-1, predicted amino acid sequence.

Sequence ID No. 3: Human Asp-2(a), nucleotide sequence.

Sequence ID No. 4: Human Asp-2(a), predicted amino acid sequence. The
30 Asp2(a) amino acid sequence includes a putative signal peptide comprising residues 1

to 21; and a putative pre-propeptide after the signal peptide that extends through residue 45 (as assessed by processing observed of recombinant Asp2(a) in CHO cells), and a putative propeptide that may extend to at least about residue 57, based on the observation of an observed GRR1GS (SEQ ID NO: 68) sequence which has characteristics of a protease recognition sequence. The Asp2(a) further includes a transmembrane domain comprising residues 455-477, a cytoplasmic domain comprising residues 478-501, and a putative alpha-helical spacer region, comprising residues 420-454, believed to be unnecessary for proteolytic activity, between the protease catalytic domain and the transmembrane domain.

10 Sequence ID No. 5: Human Asp-2(b), nucleotide sequence.

Sequence ID No. 6: Human Asp-2(b), predicted amino acid sequence. The Asp2(b) amino acid sequence includes a putative signal peptide, pre-propeptide, and propeptide as described above for Asp2(a). The Asp2(b) further includes a transmembrane domain comprising residues 430-452, a cytoplasmic domain comprising residues 453-476, and a putative alpha-helical spacer region, comprising residues 395-429, believed to be unnecessary for proteolytic activity, between the protease catalytic domain and the transmembrane domain.

15 Sequence ID No. 7: Murine Asp-2(a), nucleotide sequence.

Sequence ID No. 8: Murine Asp-2(a), predicted amino acid sequence. The proteolytic processing of murine Asp2(a) is believed to be analogous to the processing described above for human Asp2(a). In addition, a variant lacking amino acid residues 190-214 of SEQ ID NO: 8 is specifically contemplated as a murine Asp2(b) polypeptide.

20 Sequence ID No. 9: Human APP695, nucleotide sequence.

Sequence ID No. 10: Human APP695, predicted amino acid sequence.

Sequence ID No. 11: Human APP695-Sw, nucleotide sequence.

Sequence ID No. 12: Human APP695-Sw, predicted amino acid sequence. In the APP695 isoform, the Sw mutation is characterized by a KM~NL alteration at positions 595-596 (compared to normal APP695).

25 Sequence ID No. 13: Human APP695-VF, nucleotide sequence.

Sequence ID No.14: Human APP695-VF, predicted amino acid sequence. In the APP 695 isoform, the VF mutation is characterized by a V-F alteration at position 642 (compared to normal APP 695).

Sequence ID No.15: Human APP695-KK, nucleotide sequence.

5 Sequence ID No.16: Human APP695-KK, predicted amino acid sequence.
(APP695 with two carboxy-terminal lysine residues.)

Sequence ID No.17: Human APP695-Sw-KK, nucleotide sequence.

Sequence ID No.18: Human APP695-Sw-KK, predicted amino acid sequence

Sequence ID No.19: Human APP695-VF-KK, nucleotide sequence

10 Sequence ID No.20: Human APP695-VF-KK, predicted amino acid sequence

Sequence ID No.21: T7-Human-pro-Asp-2(a)ΔTM, nucleotide sequence

Sequence ID No.22: T7-Human-pro-Asp-2(a)ΔTM, amino acid sequence

Sequence ID No.23: T7-Caspase-Human-pro-Asp-2(a)ΔTM, nucleotide
sequence

15 Sequence ID No.24: T7-Caspase-Human-pro-Asp-2(a)ΔTM, amino acid
sequence

Sequence ID No.25: Human-pro-Asp-2(a)ΔTM (low GC), nucleotide
sequence

20 Sequence ID No.26: Human-pro-Asp-2(a)ΔTM, (low GC), amino acid
sequence

Sequence ID No.27: T7-Caspase-Caspase 8
cleavage-Human-pro-Asp-2(a)ΔTM, nucleotide sequence

Sequence ID No.28: T7-Caspase-Caspase 8
cleavage-Human-pro-Asp-2(a)ΔTM, amino acid sequence

25 Sequence ID No.29: Human Asp-2(a)ΔTM, nucleotide sequence

Sequence ID No.30: Human Asp-2(a)ΔTM, amino acid sequence

Sequence ID No.31: Human Asp-2(a)ΔTM(His)₆, nucleotide sequence

Sequence ID No.32: Human Asp-2(a)ΔTM(His)₆, amino acid sequence

30 Sequence ID Nos. 33-49 are short synthetic peptide and oligonucleotide
sequences that are described below in the Detailed Description of the Invention.

Sequence ID No. 50: Human Asp2(b)ΔTM polynucleotide sequence.

Sequence ID No. 51: Human Asp2(b)ΔTM polypeptide sequence (exemplary variant of Human Asp2(b) lacking transmembrane and intracellular domains of Hu-Asp2(b) set forth in SEQ ID NO: 6.

5 Sequence ID No. 52: Human Asp2(b)ΔTM(His)₆ polynucleotide sequence.

Sequence ID No. 53: Human Asp2(b)ΔTM(His)₆ polypeptide sequence (Human Asp2(b)ΔTM with six histidine tag attached to C-terminus)

Sequence ID No. 54: Human APP770-encoding polynucleotide sequence.

Sequence ID No. 55: Human APP770 polypeptide sequence. To introduce the 10 KM-NL Swedish mutation, residues KM at positions 670-71 are changed to NL. To introduce the V-F London mutation, the V residue at position 717 is changed to F.

Sequence ID No. 56: Human APP751 encoding polynucleotide sequence.

Sequence ID No. 57: Human APP751 polypeptide sequence (Human APP751 isoform).

15 Sequence ID No. 58: Human APP770-KK encoding polynucleotide sequence.

Sequence ID No. 59: Human APP770-KK polypeptide sequence. (Human APP770 isoform to which two C-terminal lysines have been added).

Sequence ID No. 60: Human APP751-KK encoding polynucleotide sequence.

Sequence ID No. 61: Human APP751-KK polypeptide sequence (Human 20 APP751 isoform to which two C-terminal lysines have been added).

Sequence ID No. 62-65: Various short peptide sequences described in detail in detailed description.

BRIEF DESCRIPTION OF THE FIGURES

25 Figure 1: Figure 1 shows the nucleotide (SEQ ID NO:1) and predicted amino acid sequence (SEQ ID NO:2) of human Asp1.

Figure 2: Figure 2 shows the nucleotide (SEQ ID NO:3) and predicted amino acid sequence (SEQ ID NO:4) of human Asp2(a).

Figure 3: Figure 3 shows the nucleotide (SEQ ID NO:5) and predicted amino acid sequence (SEQ ID NO:6) of human Asp2(b). The predicted transmembrane domain of Hu-Asp2(b) is enclosed in brackets.

5 Figure 4: Figure 4 shows the nucleotide (SEQ ID No. 7) and predicted amino acid sequence (SEQ ID No. 8) of murine Asp2(a)

Figure 5: Figure 5 shows the BestFit alignment of the predicted amino acid sequences of Hu-Asp2(a) (SEQ ID NO: 4) and murine Asp2(a) (SEQ ID NO: 8).

10 Figure 6: Figure 6 shows the nucleotide (SEQ ID No. 21) and predicted amino acid sequence (SEQ ID No. 22) of T7-Human-pro-Asp-2(a)ΔTM

Figure 7: Figure 7 shows the nucleotide (SEQ ID No. 23) and predicted amino acid sequence (SEQ ID No. 24) of T7-caspase-Human-pro-Asp-2(a)ΔTM

15 Figure 8: Figure 8 shows the nucleotide (SEQ ID No. 25) and predicted amino acid sequence (SEQ ID No. 26) of Human-pro-Asp-2(a)ΔTM (low GC)

Figure 9: Western blot showing reduction of CTF99 production by HEK125.3 cells transfected with antisense oligomers targeting the Hu-Asp2 mRNA.

20 Figure 10: Western blot showing increase in CTF99 production in mouse Neuro-2a cells cotransfected with APP-KK with and without Hu-Asp2 only in those cells cotransfected with Hu-Asp2. A further increase in CTF99 production is seen in cells cotransfected with APP-Sw-KK with and without Hu-Asp2 only in those cells cotransfected with Hu-Asp2

Figure 11: Figure 11 shows the predicted amino acid sequence (SEQ ID No. 30) of Human-Asp2(a)ΔTM

25 Figure 12: Figure 11 shows the predicted amino acid sequence (SEQ ID No. 30) of Human-Asp2(a)ΔTM(His)₆

DETAILED DESCRIPTION OF THE INVENTION

A few definitions used in this invention follow, most definitions to be used are those that would be used by one ordinarily skilled in the art.

The term "β amyloid peptide" means any peptide resulting from beta secretase cleavage of APP. This includes peptides of 39, 40, 41, 42 and 43 amino acids, extending

from the β -secretase cleavage site to 39, 40, 41, 42 and 43 amino acids C-terminal to the β -secretase cleavage site. β amyloid peptide also includes sequences 1-6, SEQ ID NOs. 1-6 of US 5,750,349, issued 12 May 1998 (incorporated into this document by reference). A β -secretase cleavage fragment disclosed here is called CTF-99, which extends from 5 β -secretase cleavage site to the carboxy terminus of APP.

When an isoform of APP is discussed then what is meant is any APP polypeptide, including APP variants (including mutations), and APP fragments that exists in humans such as those described in US 5,766,846, col 7, lines 45-67, incorporated into this document by reference.

10 The term “ β -amyloid precursor protein” (APP) as used herein is defined as a polypeptide that is encoded by a gene of the same name localized in humans on the long arm of chromosome 21 and that includes “ β AP – here “ β -amyloid protein” see above, within its carboxyl third. APP is a glycosylated, single-membrane spanning protein expressed in a wide variety of cells in many mammalian tissues. Examples of 15 specific isotypes of APP which are currently known to exist in humans are the 695 amino acid polypeptide described by Kang et. al. (1987) Nature 325:733-736 which is designated as the “normal” APP (SEQ ID NOs: 9-10); the 751 amino acid polypeptide described by Ponte et al. (1988) Nature 331:525-527 (1988) and Tanzi et al. (1988) Nature 331:528-530 (SEQ ID NOs: 56-57); and the 770-amino acid polypeptide 20 described by Kitaguchi et. al. (1988) Nature 331:530-532 (SEQ ID NOs: 54-55). Examples of specific variants of APP include point mutation which can differ in both position and phenotype (for review of known variant mutation see Hardy (1992) Nature Genet. 1:233-234). All references cited here incorporated by reference. The term “APP fragments” as used herein refers to fragments of APP other than those 25 which consist solely of β AP or β AP fragments. That is, APP fragments will include amino acid sequences of APP in addition to those which form intact β AP or a fragment of β AP.

When the term “any amino acid” is used, the amino acids referred to are to be selected from the following, three letter and single letter abbreviations - which may 30 also be used, are provided as follows:

Alanine, Ala, A; Arginine, Arg, R; Asparagine, Asn, N; Aspartic acid, Asp, D; Cysteine, Cys, C; Glutamine, Gln, Q; Glutamic Acid, Glu, E; Glycine, Gly, G; Histidine, His, H; Isoleucine, Ile, I; Leucine, Leu, L; Lysine, Lys, K; Methionine, Met, M; Phenylalanine, Phe, F; Proline, Pro, P; Serine, Ser, S; Threonine, Thr, T; 5 Tryptophan, Trp, W; Tyrosine, Tyr, Y; Valine, Val, V; Aspartic acid or Asparagine, Asx, B; Glutamic acid or Glutamine, Glx, Z; Any amino acid, Xaa, X.

The present invention describes a method to scan gene databases for the simple active site motif characteristic of aspartyl proteases. Eukaryotic aspartyl proteases such as pepsin and renin possess a two-domain structure which folds to bring two aspartyl residues into proximity within the active site. These are embedded in the short tripeptide motif DTG, or more rarely, DSG. Most aspartyl proteases occur as proenzyme whose N-terminus must be cleaved for activation. The DTG or DSG active site motif appears at about residue 65-70 in the proenzyme (prorenin, pepsinogen), but at about residue 25-30 in the active enzyme after cleavage of the N-terminal prodomain. The limited length of the active site motif makes it difficult to search collections of short, expressed sequence tags (EST) for novel aspartyl proteases. EST sequences typically average 250 nucleotides or less, and so would encode 80-90 amino acid residues or less. That would be too short a sequence to span the two active site motifs. The preferred method is to scan databases of hypothetical or assembled protein coding sequences. The present invention describes a computer method to identify candidate aspartyl proteases in protein sequence databases. The method was used to identify seven candidate aspartyl protease sequences in the *Caenorhabditis elegans* genome. These sequences were then used to identify by homology search Hu-Asp1 and two alternative splice variants of Hu-Asp2, designated 10 herein as Hu-Asp2(a) and Hu-Asp2(b).
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In a major aspect of the invention disclosed here we provide new information about APP processing. Pathogenic processing of the amyloid precursor protein (APP) via the A β pathway requires the sequential action of two proteases referred to as β -secretase and γ -secretase. Cleavage of APP by the β -secretase and γ -secretase 30 generates the N-terminus and C-terminus of the A β peptide, respectively. Because

over production of the A β peptide, particularly the A β ₁₋₄₂, has been implicated in the initiation of Alzheimer's disease, inhibitors of either the β -secretase and/or the γ -secretase have potential in the treatment of Alzheimer's disease. Despite the importance of the β -secretase and γ -secretase in the pathogenic processing of APP,
5 molecular definition of these enzymes has not been accomplished to date. That is, it was not known what enzymes were required for cleavage at either the β -secretase or the γ -secretase cleavage site. The sites themselves were known because APP was known and the A β ₁₋₄₂, peptide was known, see US 5,766,846 and US 5,837,672, (incorporated by reference, with the exception to reference to "soluble" peptides). But
10 what enzyme was involved in producing the A β ₁₋₄₂, peptide was unknown.

Alignment of the amino acid sequences of Hu-Asp2 with other known aspartyl proteases reveals a similar domain organization. All of the sequences contain a signal sequence followed by a pro-segment and the catalytic domain containing 2 copies of the aspartyl protease active site motif (DTG/DSG) separated by approximately 180
15 amino acid residues. Comparison of the processing site for proteolytic removal of the pro-segment in the mature forms of pepsin A, pepsin C, cathepsin D, cathepsin E and renin reveals that the mature forms of these enzymes contain between 31-35 amino acid residues upstream of the first DTG motif. Inspection of this region in the
Hu-Asp-2 amino acid sequence indicates a preferred processing site within the
20 sequence GRR!GS (SEQ ID NO: 68) as proteolytic processing of pro-protein precursors commonly occurs at site following dibasic amino acid pairs (eg. RR). Also, processing at this site would yield a mature enzyme with 35 amino acid residues upstream of the first DTG, consistent with the processing sites for other aspartyl proteases. In the absence of self-activation of Hu-Asp2 or a knowledge of the
25 endogenous protease that processes Hu-Asp2 at this site, a recombinant form was engineered by introducing a recognition site for the PreSission protease (LEVLFQ!GP; SEQ ID NO: 62) into the expression plasmids for bacterial, insect cell, and mammalian cell expression of pro-Hu-Asp2. In each case, the Gly residue in P1' position corresponds to the Gly residue 35 amino acids upstream of the first DTG motif in Hu-Asp2.
30

The present invention involves the molecular definition of several novel human aspartyl proteases and one of these, referred to as Hu-Asp-2(a) and Hu-Asp2(b), has been characterized in detail. Previous forms of asp1 and asp 2 have been disclosed, see EP 0848062 A2 and EP 0855444A2, inventors David Powel et al.,
5 assigned to Smith Kline Beecham Corp. (incorporated by reference). Herein are disclosed old and new forms of Hu-Asp 2. For the first time they are expressed in active form, their substrates are disclosed, and their specificity is disclosed. Prior to this disclosure cell or cell extracts were required to cleave the β -secretase site, now purified protein can be used in assays, also described here. Based on the results of (1)
10 antisense knock out experiments, (2) transient transfection knock in experiments, and (3) biochemical experiments using purified recombinant Hu-Asp-2, we demonstrate that Hu-Asp-2 is the β -secretase involved in the processing of APP. Although the nucleotide and predicted amino acid sequence of Hu-Asp-2(a) has been reported, see above, see EP 0848062 A2 and EP 0855444A2, no functional characterization of the
15 enzyme was disclosed. Here the authors characterize the Hu-Asp-2 enzyme and are able to explain why it is a critical and essential enzyme required in the formation of $A\beta_{1,42}$, peptide and possible a critical step in the development of AD.

In another embodiment the present invention also describes a novel splice variant of Hu-Asp2, referred to as Hu-Asp-2(b), that has never before been disclosed.

20 In another embodiment, the invention provides isolated nucleic acid molecules comprising a polynucleotide encoding a polypeptide selected from the group consisting of human aspartyl protease 1 (Hu-Asp1) and two alternative splice variants of human aspartyl protease-2 (Hu-Asp2), designated herein as Hu-Asp2(a) and Hu-Asp2(b). As used herein, all references to "Hu-Asp2" should be understood to refer to both Hu-Asp2(a) and Hu-Asp2(b). Hu-Asp1 is expressed most abundantly in pancreas and prostate tissues, while Hu-Asp2(a) and Hu-Asp2(b) are expressed most abundantly in pancreas and brain tissues. The invention also provides isolated Hu-Asp1, Hu-Asp2(a), and Hu-Asp2(b) polypeptides, as well as fragments thereof which exhibit aspartyl protease activity.
25

The predicted amino acid sequences of Hu-Asp1, Hu-Asp2(a) and Hu-Asp2(b) share significant homology with previously identified mammalian aspartyl proteases such as pepsinogen A, pepsinogen B, cathepsin D, cathepsin E, and renin. P.B.Szecs, *Scand. J. Clin. Lab. Invest.* 52:(Suppl. 210 5-22 (1992)). These enzymes are
5 characterized by the presence of a duplicated DTG/DSG sequence motif. The Hu-Asp1 and HuAsp2 polypeptides disclosed herein also exhibit extremely high homology with the ProSite consensus motif for aspartyl proteases extracted from the SwissProt database.

The nucleotide sequence given as residues 1-1554 of SEQ ID NO:1
10 corresponds to the nucleotide sequence encoding Hu-Asp1, the nucleotide sequence given as residues 1-1503 of SEQ ID NO:3 corresponds to the nucleotide sequence encoding Hu-Asp2(a), and the nucleotide sequence given as residues 1-1428 of SEQ ID NO:5 corresponds to the nucleotide sequence encoding Hu-Asp2(b). The isolation and sequencing of DNA encoding Hu-Asp1, Hu-Asp2(a), and Hu-Asp2(b) is
15 described below in Examples 1 and 2.

As is described in Examples 1 and 2, automated sequencing methods were used to obtain the nucleotide sequence of Hu-Asp1, Hu-Asp2(a), and Hu-Asp-2(b). The Hu-Asp nucleotide sequences of the present invention were obtained for both DNA strands, and are believed to be 100% accurate. However, as is known in the art, nucleotide sequence obtained by such automated methods may contain some errors.
20 Nucleotide sequences determined by automation are typically at least about 90%, more typically at least about 95% to at least about 99.9% identical to the actual nucleotide sequence of a given nucleic acid molecule. The actual sequence may be more precisely determined using manual sequencing methods, which are well known in the art. An error in sequence which results in an insertion or deletion of one or more nucleotides may result in a frame shift in translation such that the predicted amino acid sequence will differ from that which would be predicted from the actual nucleotide sequence of the nucleic acid molecule, starting at the point of the mutation.
25 The Hu-Asp DNA of the present invention includes cDNA, chemically synthesized DNA, DNA isolated by PCR, genomic DNA, and combinations thereof. Genomic
30

Hu-Asp DNA may be obtained by screening a genomic library with the Hu-Asp2 cDNA described herein, using methods that are well known in the art, or with oligonucleotides chosen from the Hu-Asp2 sequence that will prime the polymerase chain reaction (PCR). RNA transcribed from Hu-Asp DNA is also encompassed by
5 the present invention.

Due to the degeneracy of the genetic code, two DNA sequences may differ and yet encode identical amino acid sequences. The present invention thus provides isolated nucleic acid molecules having a polynucleotide sequence encoding any of the Hu-Asp polypeptides of the invention, wherein said polynucleotide sequence encodes
10 a Hu-Asp polypeptide having the complete amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, or fragments thereof.

Also provided herein are purified Hu-Asp polypeptides, both recombinant and non-recombinant. Most importantly, methods to produce Hu-Asp2 polypeptides in active form are provided. These include production of Hu-Asp2 polypeptides and
15 variants thereof in bacterial cells, insect cells, and mammalian cells, also in forms that allow secretion of the Hu-Asp2 polypeptide from bacterial, insect or mammalian cells into the culture medium, also methods to produce variants of Hu-Asp2 polypeptide incorporating amino acid tags that facilitate subsequent purification. In a preferred embodiment of the invention the Hu-Asp2 polypeptide is converted to a
20 proteolytically active form either in transformed cells or after purification and cleavage by a second protease in a cell-free system, such active forms of the Hu-Asp2 polypeptide beginning with the N-terminal sequence TQHGIR (SEQ ID NO: 69) or ETDEEP (SEQ ID NO: 70). The sequence TQHGIR (SEQ ID NO: 69) represents the amino-terminus of Asp2(a) or Asp2(b) beginning with residue 22 of SEQ ID NO: 4 or
25 6, after cleavage of a putative 21 residue signal peptide. Recombinant Asp2(a) expressed in and purified from insect cells was observed to have this amino terminus, presumably as a result of cleavage by a signal peptidase. The sequence ETDEEP (SEQ ID NO: 70) represents the amino-terminus of Asp2(a) or Asp2(b) beginning with residue 46 of SEQ ID NO: 4 or 6, as observed when Asp2(a) has been
30 recombinantly produced in CHO cells (presumably after cleavage by both a rodent

signal peptidase and another rodent peptidase that removes a propeptide sequence). The Asp2(a) produced in the CHO cells possesses β -secretase activity, as described in greater detail in Examples 11 and 12. Variants and derivatives, including fragments, of Hu-Asp proteins having the native amino acid sequences given in SEQ ID Nos: 2, 5 4, and 6 that retain any of the biological activities of Hu-Asp are also within the scope of the present invention. Of course, one of ordinary skill in the art will readily be able to determine whether a variant, derivative, or fragment of a Hu-Asp protein displays Hu-Asp activity by subjecting the variant, derivative, or fragment to a standard aspartyl protease assay. Fragments of Hu-Asp within the scope of this invention 10 include those that contain the active site domain containing the amino acid sequence DTG, fragments that contain the active site domain amino acid sequence DSG, fragments containing both the DTG and DSG active site sequences, fragments in which the spacing of the DTG and DSG active site sequences has been lengthened, fragments in which the spacing has been shortened. Also within the scope of the 15 invention are fragments of Hu-Asp in which the transmembrane domain has been removed to allow production of Hu-Asp2 in a soluble form. In another embodiment of the invention, the two halves of Hu-Asp2, each containing a single active site DTG or DSG sequence can be produced independently as recombinant polypeptides, then combined in solution where they reconstitute an active protease.

20 Thus, the invention provides a purified polypeptide comprising a fragment of a mammalian Asp2 protein, wherein said fragment lacks the Asp2 transmembrane domain of said Asp2 protein, and wherein the polypeptide and the fragment retain the β -secretase activity of said mammalian Asp2 protein. In a preferred embodiment, the purified polypeptide comprises a fragment of a human Asp2 protein that retains the β -secretase activity of the human Asp2 protein from which it was derived. Examples 25 include:

a purified polypeptide that comprises a fragment of Asp2(a) having the amino acid sequence set forth in SEQ ID NO: 4, wherein the polypeptide lacks transmembrane domain amino acids 455 to 477 of SEQ ID NO: 4;

a purified polypeptide as described in the preceding paragraph that further lacks cytoplasmic domain amino acids 478 to 501 of SEQ ID NO: 4;

5 a purified polypeptide as described in either of the preceding paragraphs that further lacks amino acids 420-454 of SEQ ID NO: 4, which constitute a putative alpha helical region between the catalytic domain and the transmembrane domain that is believed to be unnecessary for β -secretase activity;

10 a purified polypeptide that comprises an amino acid sequence that includes amino acids 58 to 419 of SEQ ID NO: 4, and that lacks amino acids 22 to 57 of SEQ ID NO: 4;

15 a purified polypeptide that comprises an amino acid sequence that includes amino acids 46 to 419 of SEQ ID NO: 4, and that lacks amino acids 22 to 45 of SEQ ID NO: 4;

20 a purified polypeptide that comprises an amino acid sequence that includes amino acids 22 to 454 of SEQ ID NO: 4.

25 a purified polypeptide that comprises a fragment of Asp2(b) having the amino acid sequence set forth in SEQ ID NO: 6, and wherein said polypeptide lacks transmembrane domain amino acids 430 to 452 of SEQ ID NO: 6;

a purified polypeptide as described in the preceding paragraph that further lacks cytoplasmic domain amino acids 453 to 476 of SEQ ID NO: 6;

25 a purified polypeptide as described in either of the preceding two paragraphs that further lacks amino acids 395-429 of SEQ ID NO: 4, which constitute a putative alpha helical region between the catalytic domain and the transmembrane domain that is believed to be unnecessary for β -secretase activity;

a purified polypeptide comprising an amino acid sequence that includes amino acids 58 to 394 of SEQ ID NO: 4, and that lacks amino acids 22 to 57 of SEQ ID NO: 4;

a purified polypeptide comprising an amino acid sequence that includes amino acids 46 to 394 of SEQ ID NO: 4, and that lacks amino acids 22 to 45 of SEQ ID NO: 4; and

5 a purified polypeptide comprising an amino acid sequence that includes amino acids 22 to 429 of SEQ ID NO: 4.

Also included as part of the invention is a purified polynucleotide comprising a nucleotide sequence that encodes such polypeptides; a vector comprising a polynucleotide that encodes such polypeptides; and a host cell transformed or transfected with such a polynucleotide or vector.

10 Hu-Asp variants may be obtained by mutation of native Hu-Asp-encoding nucleotide sequences, for example. A Hu-Asp variant, as referred to herein, is a polypeptide substantially homologous to a native Hu-Asp polypeptide but which has an amino acid sequence different from that of native Hu-Asp because of one or more deletions, insertions, or substitutions in the amino acid sequence. The variant amino acid or nucleotide sequence is preferably at least about 80% identical, more 15 preferably at least about 90% identical, and most preferably at least about 95% identical, to a native Hu-Asp sequence. Thus, a variant nucleotide sequence which contains, for example, 5 point mutations for every one hundred nucleotides, as compared to a native Hu-Asp gene, will be 95% identical to the native protein. The 20 percentage of sequence identity, also termed homology, between a native and a variant Hu-Asp sequence may also be determined, for example, by comparing the two sequences using any of the computer programs commonly employed for this purpose, such as the Gap program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, Madison Wisconsin), which 25 uses the algorithm of Smith and Waterman (*Adv. Appl. Math.* 2: 482-489 (1981)).

Alterations of the native amino acid sequence may be accomplished by any of a number of known techniques. For example, mutations may be introduced at particular locations by procedures well known to the skilled artisan, such as oligonucleotide-directed mutagenesis, which is described by Walder *et al.* (*Gene* 30:133 (1986)); Bauer *et al.* (*Gene* 37:73 (1985)); Craik (*BioTechniques*, January

1985, pp. 12-19); Smith *et al.* (*Genetic Engineering: Principles and Methods*, Plenum Press (1981)); and U.S. Patent Nos. 4,518,584 and 4,737,462.

Hu-Asp variants within the scope of the invention may comprise conservatively substituted sequences, meaning that one or more amino acid residues of a Hu-Asp polypeptide are replaced by different residues that do not alter the secondary and/or tertiary structure of the Hu-Asp polypeptide. Such substitutions may include the replacement of an amino acid by a residue having similar physicochemical properties, such as substituting one aliphatic residue (Ile, Val, Leu or Ala) for another, or substitution between basic residues Lys and Arg, acidic residues Glu and Asp, amide residues Gln and Asn, hydroxyl residues Ser and Tyr, or aromatic residues Phe and Tyr. Further information regarding making phenotypically silent amino acid exchanges may be found in Bowie *et al.*, *Science* 247:1306-1310 (1990). Other Hu-Asp variants which might retain substantially the biological activities of Hu-Asp are those where amino acid substitutions have been made in areas outside functional regions of the protein.

In another aspect, the invention provides an isolated nucleic acid molecule comprising a polynucleotide which hybridizes under stringent conditions to a portion of the nucleic acid molecules described above, *e.g.*, to at least about 15 nucleotides, preferably to at least about 20 nucleotides, more preferably to at least about 30 nucleotides, and still more preferably to at least about from 30 to at least about 100 nucleotides, of one of the previously described nucleic acid molecules. Such portions of nucleic acid molecules having the described lengths refer to, *e.g.*, at least about 15 contiguous nucleotides of the reference nucleic acid molecule. By stringent hybridization conditions is intended overnight incubation at about 42°C for about 2.5 hours in 6 X SSC/0.1% SDS, followed by washing of the filters four times for 15 minutes in 1.0 X SSC at 65°C, 0.1% SDS.

Fragments of the Hu-Asp encoding nucleic acid molecules described herein, as well as polynucleotides capable of hybridizing to such nucleic acid molecules may be used as a probe or as primers in a polymerase chain reaction (PCR). Such probes may be used, *e.g.*, to detect the presence of Hu-Asp nucleic acids in *in vitro* assays, as well

as in Southern and northern blots. Cell types expressing Hu-Asp may also be identified by the use of such probes. Such procedures are well known, and the skilled artisan will be able to choose a probe of a length suitable to the particular application. For PCR, 5' and 3' primers corresponding to the termini of a desired Hu-Asp nucleic acid molecule are employed to isolate and amplify that sequence using conventional techniques.

Other useful fragments of the Hu-Asp nucleic acid molecules are antisense or sense oligonucleotides comprising a single stranded nucleic acid sequence capable of binding to a target Hu-Asp mRNA (using a sense strand), or Hu-Asp DNA (using an antisense strand) sequence. In a preferred embodiment of the invention these Hu-Asp antisense oligonucleotides reduce Hu-Asp mRNA and consequent production of Hu-Asp polypeptides.

In another aspect, the invention includes Hu-Asp polypeptides with or without associated native pattern glycosylation. Both Hu-Asp1 and Hu-Asp2 have canonical acceptor sites for Asn-linked sugars, with Hu-Asp1 having two of such sites, and Hu-Asp2 having four. Hu-Asp expressed in yeast or mammalian expression systems (discussed below) may be similar to or significantly different from a native Hu-Asp polypeptide in molecular weight and glycosylation pattern. Expression of Hu-Asp in bacterial expression systems will provide non-glycosylated Hu-Asp.

The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. Hu-Asp polypeptides may be recovered and purified from tissues, cultured cells, or recombinant cell cultures by well-known methods, including ammonium sulfate or ethanol precipitation, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography, lectin chromatography, and high performance liquid chromatography (HPLC). In a preferred embodiment, an amino acid tag is added to the Hu-Asp polypeptide using genetic engineering techniques that are well known to practitioners of the art which include addition of six histidine amino acid residues to allow purification by binding to nickel immobilized on a suitable support, epitopes for

polyclonal or monoclonal antibodies including but not limited to the T7 epitope, the myc epitope, and the V5a epitope, and fusion of Hu-Asp2 to suitable protein partners including but not limited to glutathione-S-transferase or maltose binding protein. In a preferred embodiment these additional amino acid sequences are added to the

5 C-terminus of Hu-Asp but may be added to the N-terminus or at intervening positions within the Hu-Asp2 polypeptide.

The present invention also relates to vectors comprising the polynucleotide molecules of the invention, as well as host cell transformed with such vectors. Any of the polynucleotide molecules of the invention may be joined to a vector, which

10 generally includes a selectable marker and an origin of replication, for propagation in a host. Because the invention also provides Hu-Asp polypeptides expressed from the polynucleotide molecules described above, vectors for the expression of Hu-Asp are preferred. The vectors include DNA encoding any of the Hu-Asp polypeptides described above or below, operably linked to suitable transcriptional or translational

15 regulatory sequences, such as those derived from a mammalian, microbial, viral, or insect gene. Examples of regulatory sequences include transcriptional promoters, operators, or enhancers, mRNA ribosomal binding sites, and appropriate sequences which control transcription and translation. Nucleotide sequences are operably linked when the regulatory sequence functionally relates to the DNA encoding Hu-Asp.

20 Thus, a promoter nucleotide sequence is operably linked to a Hu-Asp DNA sequence if the promoter nucleotide sequence directs the transcription of the Hu-Asp sequence.

Selection of suitable vectors to be used for the cloning of polynucleotide molecules encoding Hu-Asp, or for the expression of Hu-Asp polypeptides, will of course depend upon the host cell in which the vector will be transformed, and, where applicable, the host cell from which the Hu-Asp polypeptide is to be expressed.

25 Suitable host cells for expression of Hu-Asp polypeptides include prokaryotes, yeast, and higher eukaryotic cells, each of which is discussed below.

The Hu-Asp polypeptides to be expressed in such host cells may also be fusion proteins which include regions from heterologous proteins. Such regions may be included to allow, e.g., secretion, improved stability, or facilitated purification of the

polypeptide. For example, a sequence encoding an appropriate signal peptide can be incorporated into expression vectors. A DNA sequence for a signal peptide (secretory leader) may be fused inframe to the Hu-Asp sequence so that Hu-Asp is translated as a fusion protein comprising the signal peptide. A signal peptide that is functional in the intended host cell promotes extracellular secretion of the Hu-Asp polypeptide.

5 Preferably, the signal sequence will be cleaved from the Hu-Asp polypeptide upon secretion of Hu-Asp from the cell. Nonlimiting examples of signal sequences that can be used in practicing the invention include the yeast Ifactor and the honeybee melatin leader in sf9 insect cells.

10 In a preferred embodiment, the Hu-Asp polypeptide will be a fusion protein which includes a heterologous region used to facilitate purification of the polypeptide. Many of the available peptides used for such a function allow selective binding of the fusion protein to a binding partner. For example, the Hu-Asp polypeptide may be modified to comprise a peptide to form a fusion protein which specifically binds to a 15 binding partner, or peptide tag. Nonlimiting examples of such peptide tags include the 6-His tag, thioredoxin tag, hemagglutinin tag, GST tag, and OmpA signal sequence tag. As will be understood by one of skill in the art, the binding partner which recognizes and binds to the peptide may be any molecule or compound including metal ions (e.g., metal affinity columns), antibodies, or fragments thereof, and any protein or peptide 20 which binds the peptide, such as the FLAG tag.

Suitable host cells for expression of Hu-Asp polypeptides includes prokaryotes, yeast, and higher eukaryotic cells. Suitable prokaryotic hosts to be used for the expression of Hu-Asp include bacteria of the genera *Escherichia*, *Bacillus*, and *Salmonella*, as well as members of the genera *Pseudomonas*, *Streptomyces*, and 25 *Staphylococcus*. For expression in, e.g., *E. coli*, a Hu-Asp polypeptide may include an N-terminal methionine residue to facilitate expression of the recombinant polypeptide in a prokaryotic host. The N-terminal Met may optionally then be cleaved from the expressed Hu-Asp polypeptide. Other N-terminal amino acid residues can be added to the Hu-Asp polypeptide to facilitate expression in 30 *Escherichia coli* including but not limited to the T7 leader sequence, the T7-caspase 8

leader sequence, as well as others leaders including tags for purification such as the 6-His tag (Example 9). Hu-Asp polypeptides expressed in *E. coli* may be shortened by removal of the cytoplasmic tail, the transmembrane domain, or the membrane proximal region. Hu-Asp polypeptides expressed in *E. coli* may be obtained in either 5 a soluble form or as an insoluble form which may or may not be present as an inclusion body. The insoluble polypeptide may be rendered soluble by guanidine HCl, urea or other protein denaturants, then refolded into a soluble form before or after purification by dilution or dialysis into a suitable aqueous buffer. If the inactive proform of the Hu-Asp was produced using recombinant methods, it may be rendered 10 active by cleaving off the prosegment with a second suitable protease such as human immunodeficiency virus protease.

Expression vectors for use in prokaryotic hosts generally comprises one or more phenotypic selectable marker genes. Such genes generally encode, e.g., a protein that confers antibiotic resistance or that supplies an auxotrophic requirement. 15 A wide variety of such vectors are readily available from commercial sources. Examples include pSPORT vectors, pGEM vectors (Promega), pPROEX vectors (LTI, Bethesda, MD), Bluescript vectors (Stratagene), pET vectors (Novagen) and pQE vectors (Qiagen).

Hu-Asp may also be expressed in yeast host cells from genera including 20 *Saccharomyces*, *Pichia*, and *Kluveromyces*. Preferred yeast hosts are *S. cerevisiae* and *P. pastoris*. Yeast vectors will often contain an origin of replication sequence from a 2T yeast plasmid, an autonomously replicating sequence (ARS), a promoter region, sequences for polyadenylation, sequences for transcription termination, and a selectable marker gene. Vectors replicable in both yeast and *E. coli* (termed shuttle 25 vectors) may also be used. In addition to the above-mentioned features of yeast vectors, a shuttle vector will also include sequences for replication and selection in *E. coli*. Direct secretion of Hu-Asp polypeptides expressed in yeast hosts may be accomplished by the inclusion of nucleotide sequence encoding the yeast I-factor leader sequence at the 5' end of the Hu-Asp-encoding nucleotide sequence.

Insect host cell culture systems may also be used for the expression of Hu-Asp polypeptides. In a preferred embodiment, the Hu-Asp polypeptides of the invention are expressed using an insect cell expression system (see Example 10). Additionally, a baculovirus expression system can be used for expression in insect cells as reviewed by Luckow and Summers, *Bio/Technology* 6:47 (1988).

5 In another preferred embodiment, the Hu-Asp polypeptide is expressed in mammalian host cells. Nonlimiting examples of suitable mammalian cell lines include the COS7 line of monkey kidney cells (Gluzman *et al.*, *Cell* 23:175 (1981)), human embryonic kidney cell line 293, and Chinese hamster ovary (CHO) cells.

10 Preferably, Chinese hamster ovary (CHO) cells are used for expression of Hu-Asp proteins (Example 11).

The choice of a suitable expression vector for expression of the Hu-Asp polypeptides of the invention will of course depend upon the specific mammalian host cell to be used, and is within the skill of the ordinary artisan. Examples of suitable 15 expression vectors include pcDNA3 (Invitrogen) and pSVL (Pharmacia Biotech). A preferred vector for expression of Hu-Asp polypeptides is pcDNA3.1-Hygro (Invitrogen). Expression vectors for use in mammalian host cells may include transcriptional and translational control sequences derived from viral genomes. Commonly used promoter sequences and enhancer sequences which may be used in 20 the present invention include, but are not limited to, those derived from human cytomegalovirus (CMV), Adenovirus 2, Polyoma virus, and Simian virus 40 (SV40). Methods for the construction of mammalian expression vectors are disclosed, for example, in Okayama and Berg (*Mol. Cell. Biol.* 3:280 (1983)); Cosman *et al.* (*Mol. Immunol.* 23:935 (1986)); Cosman *et al.* (*Nature* 312:768 (1984)); EP-A-0367566; 25 and WO 91/18982.

The polypeptides of the present invention may also be used to raise polyclonal and monoclonal antibodies, which are useful in diagnostic assays for detecting Hu-Asp polypeptide expression. Such antibodies may be prepared by conventional techniques. See, for example, *Antibodies: A Laboratory Manual*, Harlow and Land 30 (eds.), Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., (1988);

Monoclonal Antibodies, Hybridomas: A New Dimension in Biological Analyses,
Kennet et al. (eds.), Plenum Press, New York (1980). Synthetic peptides comprising
portions of Hu-Asp containing 5 to 20 amino acids may also be used for the
production of polyclonal or monoclonal antibodies after linkage to a suitable carrier
5 protein including but not limited to keyhole limpet hemacyanin (KLH), chicken
ovalbumin, or bovine serum albumin using various cross-linking reagents including
carbodiimides, glutaraldehyde, or if the peptide contains a cysteine,
N-methylmaleimide. A preferred peptide for immunization when conjugated to KLH
contains the C-terminus of Hu-Asp1 or Hu-Asp2 comprising
10 QRRPRDPEVVNDESSLVRHRWK (SEQ ID NO: 2, residues 497-518) or
LRQQHDDFADDISLLK (SEQ ID NO:4, residues 486-501), respectively. See SEQ
ID Nos. 33-34.

The Hu-Asp nucleic acid molecules of the present invention are also valuable
for chromosome identification, as they can hybridize with a specific location on a
15 human chromosome. Hu-Asp1 has been localized to chromosome 21, while
Hu-Asp2 has been localized to chromosome 11q23.3-24.1. There is a current need for
identifying particular sites on the chromosome, as few chromosome marking reagents
based on actual sequence data (repeat polymorphisms) are presently available for
marking chromosomal location. Once a sequence has been mapped to a precise
20 chromosomal location, the physical position of the sequence on the chromosome can
be correlated with genetic map data. The relationship between genes and diseases that
have been mapped to the same chromosomal region can then be identified through
linkage analysis, wherein the coinheritance of physically adjacent genes is determined.
Whether a gene appearing to be related to a particular disease is in fact the cause of
25 the disease can then be determined by comparing the nucleic acid sequence between
affected and unaffected individuals.

In another embodiment, the invention relates to a method of assaying Hu-Asp
function, specifically Hu-Asp2 function which involves incubating in solution the
Hu-Asp polypeptide with a suitable substrate including but not limited to a synthetic
30 peptide containing the β -secretase cleavage site of APP, preferably one containing the

mutation found in a Swedish kindred with inherited AD in which KM is changed to NL, such peptide comprising the sequence SEVNLDAEFR (SEQ ID NO: 63) in an acidic buffering solution, preferably an acidic buffering solution of pH5.5 (see Example 12) using cleavage of the peptide monitored by high performance liquid chromatography as a measure of Hu-Asp proteolytic activity. Preferred assays for proteolytic activity utilize internally quenched peptide assay substrates. Such suitable substrates include peptides which have attached a paired fluorophore and quencher including but not limited to 7-amino-4-methyl coumarin and dinitrophenol, respectively, such that cleavage of the peptide by the Hu-Asp results in increased fluorescence due to physical separation of the fluorophore and quencher. Other paired fluorophores and quenchers include bodipy-tetramethylrhodamine and QSY-5 (Molecular Probes, Inc.). In a variant of this assay, biotin or another suitable tag may be placed on one end of the peptide to anchor the peptide to a substrate assay plate and a fluorophore may be placed at the other end of the peptide. Useful fluorophores include those listed above as well as Europium labels such as W8044 (EG&g Wallac, Inc.). Cleavage of the peptide by Asp2 will release the fluorophore or other tag from the plate, allowing compounds to be assayed for inhibition of Asp2 proteolytic cleavage as shown by an increase in retained fluorescence. Preferred colorimetric assays of Hu-Asp proteolytic activity utilize other suitable substrates that include the P2 and P1 amino acids comprising the recognition site for cleavage linked to o-nitrophenol through an amide linkage, such that cleavage by the Hu-Asp results in an increase in optical density after altering the assay buffer to alkaline pH.

In another embodiment, the invention relates to a method for the identification of an agent that increases the activity of a Hu-Asp polypeptide selected from the group consisting of Hu-Asp1, Hu-Asp2(a), and Hu-Asp2(b), the method comprising

- (a) determining the activity of said Hu-Asp polypeptide in the presence of a test agent and in the absence of a test agent; and
- (b) comparing the activity of said Hu-Asp polypeptide determined in the presence of said test agent to the activity of said Hu-Asp polypeptide determined in the absence of said test agent;

whereby a higher level of activity in the presence of said test agent than in the absence of said test agent indicates that said test agent has increased the activity of said Hu-Asp polypeptide. Such tests can be performed with Hu-Asp polypeptide in a cell free system and with cultured cells that express Hu-Asp as well as variants or isoforms thereof.

5 In another embodiment, the invention relates to a method for the identification of an agent that decreases the activity of a Hu-Asp polypeptide selected from the group consisting of Hu-Asp1, Hu-Asp2(a), and Hu-Asp2(b), the method comprising

10 (a) determining the activity of said Hu-Asp polypeptide in the presence of a test agent and in the absence of a test agent; and

(b) comparing the activity of said Hu-Asp polypeptide determined in the presence of said test agent to the activity of said Hu-Asp polypeptide determined in the absence of said test agent;

15 whereby a lower level of activity in the presence of said test agent than in the absence of said test agent indicates that said test agent has decreased the activity of said Hu-Asp polypeptide. Such tests can be performed with Hu-Asp polypeptide in a cell free system and with cultured cells that express Hu-Asp as well as variants or isoforms thereof.

20 In another embodiment, the invention relates to a novel cell line (HEK125.3 cells) for measuring processing of amyloid β peptide ($A\beta$) from the amyloid protein precursor (APP). The cells are stable transformants of human embryonic kidney 293 cells (HEK293) with a bicistronic vector derived from pIRES-EGFP (Clontech) containing a modified human APP cDNA, an internal ribosome entry site and an enhanced green fluorescent protein (EGFP) cDNA in the second cistron. The APP cDNA was modified by adding two lysine codons to the carboxyl terminus of the APP coding sequence. This increases processing of $A\beta$ peptide from human APP by 2-4 fold. This level of $A\beta$ peptide processing is 60 fold higher than is seen in nontransformed HEK293 cells. HEK125.3 cells will be useful for assays of compounds that inhibit $A\beta$ peptide processing. This invention also includes addition 25 of two lysine residues to the C-terminus of other APP isoforms including the 751 and

770 amino acid isoforms, to isoforms of APP having mutations found in human AD including the Swedish KM-NL and V717-F mutations, to C-terminal fragments of APP, such as those beginning with the β -secretase cleavage site, to C-terminal fragments of APP containing the β -secretase cleavage site which have been operably linked to an N-terminal signal peptide for membrane insertion and secretion, and to C-terminal fragments of APP which have been operably linked to an N-terminal signal peptide for membrane insertion and secretion and a reporter sequence including but not limited to green fluorescent protein or alkaline phosphatase, such that β -secretase cleavage releases the reporter protein from the surface of cells expressing the polypeptide.

Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of illustration and are not intended as limiting.

15

Example 1

Development of a Search Algorithm Useful for the Identification of Aspartyl Proteases, and Identification of *C. elegans* Aspartyl Protease Genes in Wormpep 12

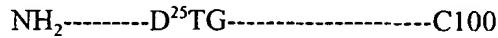
Materials and Methods:

20 Classical aspartyl proteases such as pepsin and renin possess a two-domain structure which folds to bring two aspartyl residues into proximity within the active site. These are embedded in the short tripeptide motif DTG, or more rarely, DSG. The DTG or DSG active site motif appears at about residue 25-30 in the enzyme, but at about 65-70 in the proenzyme (prorenin, pepsinogen). This motif appears again about 25 150-200 residues downstream. The proenzyme is activated by cleavage of the N-terminal prodomain. This pattern exemplifies the double domain structure of the modern day aspartyl enzymes which apparently arose by gene duplication and divergence. Thus;



30 where X denotes the beginning of the enzyme, following the N-terminal prodomain, and Y denotes the center of the molecule where the gene repeat begins again.

In the case of the retroviral enzymes such as the HIV protease, they represent only a half of the two-domain structures of well-known enzymes like pepsin, cathepsin D, renin, etc. They have no prosegment, but are carved out of a polyprotein precursor containing the *gag* and *pol* proteins of the virus. They can be represented by:



This "monomer" only has about 100 aa, so is extremely parsimonious as compared to the other aspartyl protease "dimers" which have of the order of 330 or so aa, not counting the N-terminal prodomain.

The limited length of the eukaryotic aspartyl protease active site motif makes it difficult to search EST collections for novel sequences. EST sequences typically average 250 nucleotides, and so in this case would be unlikely to span both aspartyl protease active site motifs. Instead, we turned to the *C. elegans* genome. The *C. elegans* genome is estimated to contain around 13,000 genes. Of these, roughly 12,000 have been sequenced and the corresponding hypothetical open reading frame (ORF) has been placed in the database Wormpep12. We used this database as the basis for a whole genome scan of a higher eukaryote for novel aspartyl proteases, using an algorithm that we developed specifically for this purpose. The following AWK script for locating proteins containing two DTG or DSG motifs was used for the search, which was repeated four times to recover all pairwise combinations of the aspartyl motif.

```
BEGIN{RS=">"}           /* defines ">" as record separator for FASTA format */
{
pos = index($0,"DTG")    /*finds "DTG" in record*/
if (pos>0) {
    rest = substr($0,pos+3)      /*get rest of record after first DTG*/
    pos2 = index(rest,"DTG")    /*find second DTG*/
    if (pos2>0) printf ("%s%s\n",">>",$0)      /*report hits*/
}
}

```

The AWK script shown above was used to search Wormpep12, which was downloaded from [ftp.sanger.ac.uk/pub/databases/wormpep](ftp://ftp.sanger.ac.uk/pub/databases/wormpep), for sequence entries

containing at least two DTG or DSG motifs. Using AWK limited each record to 3000 characters or less. Thus, 35 or so larger records were eliminated manually from Wormpep12 as in any case these were unlikely to encode aspartyl proteases.

Results and Discussion:

5 The Wormpep 12 database contains 12,178 entries, although some of these (<10%) represent alternatively spliced transcripts from the same gene. Estimates of the number of genes encoded in the *C. elegans* genome is on the order of 13,000 genes, so Wormpep12 may be estimated to cover greater than 90% of the *C. elegans* genome.

10 Eukaryotic aspartyl proteases contain a two-domain structure, probably arising from ancestral gene duplication. Each domain contains the active site motif D(S/T)G located from 20-25 amino acid residues into each domain. The retroviral (e.g., HIV protease) or retrotransposon proteases are homodimers of subunits which are homologous to a single eukaryotic aspartyl protease domain. An AWK script was

15 used to search the Wormpep12 database for proteins in which the D(S/T)G motif occurred at least twice. This identified >60 proteins with two DTG or DSG motifs. Visual inspection was used to select proteins in which the position of the aspartyl domains was suggestive of a two-domain structure meeting the criteria described above.

20 In addition, the PROSITE eukaryotic and viral aspartyl protease active site pattern PS00141 was used to search Wormpep12 for candidate aspartyl proteases. (Bairoch A., Bucher P., Hofmann K., The PROSITE database: its status in 1997, *Nucleic Acids Res.* 24:217-221(1997)). This generated an overlapping set of Wormpep12 sequences. Of these, seven sequences contained two DTG or DSG motifs and the PROSITE aspartyl protease active site pattern. Of these seven, three were found in the same cosmid clone (F21F8.3, F21F8.4, and F21F8.7) suggesting that they represent a family of proteins that arose by ancestral gene duplication. Two other ORFs with extensive homology to F21F8.3, F21F8.4 and F21F8.7 are present in the same gene cluster (F21F8.2 and F21F8.6), however, these contain only a single

25 DTG motif. Exhaustive BLAST searches with these seven sequences against

Wormpep12 failed to reveal additional candidate aspartyl proteases in the *C. elegans* genome containing two repeats of the DTG or DSG motif.

BLASTX search with each *C. elegans* sequence against SWISS-PROT, GenPep and TREMBL revealed that R12H7.2 was the closest worm homologue to the known mammalian aspartyl proteases, and that T18H9.2 was somewhat more distantly related, while CEASP1, F21F8.3, F21F8.4, and F21F8.7 formed a subcluster which had the least sequence homology to the mammalian sequences.
5

Discussion:

APP, the presenilins, and p35, the activator of cdk5, all undergo intracellular proteolytic processing at sites which conform to the substrate specificity of the HIV protease. Dysregulation of a cellular aspartyl protease with the same substrate specificity, might therefore provide a unifying mechanism for causation of the plaque and tangle pathologies in AD. Therefore, we sought to identify novel human aspartyl proteases. A whole genome scan in *C. elegans* identified seven open reading frames that adhere to the aspartyl protease profile that we had identified. These seven aspartyl proteases probably comprise the complete complement of such proteases in a simple, multicellular eukaryote. These include four closely related aspartyl proteases unique to *C. elegans* which probably arose by duplication of an ancestral gene. The other three candidate aspartyl proteases (T18H9.2, R12H7.2 and C11D2.2) were found to have homology to mammalian gene sequences.
10
15
20

Example 2

Identification of Novel Human Aspartyl Proteases Using Database Mining by Genome Bridging

25

Materials and Methods:

Computer-assisted analysis of EST databases, cDNA , and predicted polypeptide sequences:

Exhaustive homology searches of EST databases with the CEASP1, F21F8.3, F21F8.4, and F21F8.7 sequences failed to reveal any novel mammalian homologues.
30
TBLASTN searches with R12H7.2 showed homology to cathepsin D, cathepsin E,

pepsinogen A, pepsinogen C and renin, particularly around the DTG motif within the active site, but also failed to identify any additional novel mammalian aspartyl proteases. This indicates that the *C. elegans* genome probably contains only a single lysosomal aspartyl protease which in mammals is represented by a gene family that arose through duplication and consequent modification of an ancestral gene.

TBLASTN searches with T18H9.2, the remaining *C. elegans* sequence, identified several ESTs which assembled into a contig encoding a novel human aspartyl protease (Hu-ASP1). As is described above in Example 1, BLASTX search with the Hu-ASP1 contig against SWISS-PROT revealed that the active site motifs in the sequence aligned with the active sites of other aspartyl proteases. Exhaustive, repetitive rounds of BLASTN searches against LifeSeq, LifeSeqFL, and the public EST collections identified 102 EST from multiple cDNA libraries that assembled into a single contig. The 51 sequences in this contig found in public EST collections also have been assembled into a single contig (THC213329) by The Institute for Genome Research (TIGR). The TIGR annotation indicates that they failed to find any hits in the database for the contig. Note that the TIGR contig is the reverse complement of the LifeSeq contig that we assembled. BLASTN search of Hu-ASP1 against the rat and mouse EST sequences in ZooSeq revealed one homologous EST in each database (Incyte clone 700311523 and IMAGE clone 313341, GenBank accession number W10530, respectively).

TBLASTN searches with the assembled DNA sequence for Hu-ASP1 against both LifeSeqFL and the public EST databases identified a second, related human sequence (Hu-Asp2) represented by a single EST (2696295). Translation of this partial cDNA sequence reveals a single DTG motif which has homology to the active site motif of a bovine aspartyl protease, NM1.

BLAST searches, contig assemblies and multiple sequence alignments were performed using the bioinformatics tools provided with the LifeSeq, LifeSeqFL and LifeSeq Assembled databases from Incyte. Predicted protein motifs were identified using either the ProSite dictionary (Motifs in GCG 9) or the Pfam database.

Full-length cDNA cloning of Hu-Asp1

The open reading frame of *C. elegans* gene T18H9.2CE was used to query Incyte LifeSeq and LifeSeq-FL databases and a single electronic assembly referred to as 1863920CE1 was detected. The 5' most cDNA clone in this contig, 1863920, was obtained from Incyte and completely sequenced on both strands. Translation of the open reading frame contained within clone 1863920 revealed the presence of the duplicated aspartyl protease active site motif (DTG/DSG) but the 5' end was incomplete. The remainder of the Hu-Asp1 coding sequence was determined by 5' Marathon RACE analysis using a human placenta Marathon ready cDNA template (Clontech). A 3'-antisense oligonucleotide primer specific for the 5' end of clone 1863920 was paired with the 5'-sense primer specific for the Marathon ready cDNA synthetic adaptor in the PCR. Specific PCR products were directly sequenced by cycle sequencing and the resulting sequence assembled with the sequence of clone 1863920 to yield the complete coding sequence of Hu-Asp-1 (SEQ ID No. 1).

Several interesting features are present in the primary amino acid sequence of Hu-Asp1 (Figure 1, SEQ ID No. 2). The sequence contains a signal peptide (residues 1-20 in SEQ ID No. 2), a pro-segment, and a catalytic domain containing two copies of the aspartyl protease active site motif (DTG/DSG). The spacing between the first and second active site motifs is about 200 residues which should correspond to the expected size of a single, eukaryotic aspartyl protease domain. More interestingly, the sequence contains a predicted transmembrane domain (residues 469-492 in SEQ ID No.2) near its C-terminus which suggests that the protease is anchored in the membrane. This feature is not found in any other aspartyl protease.

25 *Cloning of a full-length Hu-Asp-2 cDNAs:*

As is described above in Example 1, genome wide scan of the *Caenorhabditis elegans* database WormPep12 for putative aspartyl proteases and subsequent mining of human EST databases revealed a human ortholog to the *C. elegans* gene T18H9.2 referred to as Hu-Asp1. The assembled contig for Hu-Asp1 was used to query for 30 human paralogs using the BLAST search tool in human EST databases and a single

significant match (2696295CE1) with approximately 60% shared identity was found in the LifeSeq FL database. Similar queries of either gb105PubEST or the family of human databases available from TIGR did not identify similar EST clones. cDNA clone 2696295, identified by single pass sequence analysis from a human uterus cDNA library, was obtained from Incyte and completely sequenced on both strands. This clone contained an incomplete 1266 bp open-reading frame that encoded a 422 amino acid polypeptide but lacked an initiator ATG on the 5' end. Inspection of the predicted sequence revealed the presence of the duplicated aspartyl protease active site motif DTG/DSG, separated by 194 amino acid residues. Subsequent queries of later releases of the LifeSeq EST database identified an additional ESTs, sequenced from a human astrocyte cDNA library (4386993), that appeared to contain additional 5' sequence relative to clone 2696295. Clone 4386993 was obtained from Incyte and completely sequenced on both strands. Comparative analysis of clone 4386993 and clone 2696295 confirmed that clone 4386993 extended the open-reading frame by 31 amino acid residues including two in-frame translation initiation codons. Despite the presence of the two in-frame ATGs, no in-frame stop codon was observed upstream of the ATG indicating that the 4386993 may not be full-length. Furthermore, alignment of the sequences of clones 2696295 and 4386993 revealed a 75 base pair insertion in clone 2696295 relative to clone 4386993 that results in the insertion of 25 additional amino acid residues in 2696295. The remainder of the Hu-Asp2 coding sequence was determined by 5' Marathon RACE analysis using a human hippocampus Marathon ready cDNA template (Clontech). A 3'-antisense oligonucleotide primer specific for the shared 5'-region of clones 2696295 and 4386993 was paired with the 5'-sense primer specific for the Marathon ready cDNA synthetic adaptor in the PCR. Specific PCR products were directly sequenced by cycle sequencing and the resulting sequence assembled with the sequence of clones 2696295 and 4386993 to yield the complete coding sequence of Hu-Asp2(a) (SEQ ID No. 3) and Hu-Asp2(b) (SEQ ID No. 5), respectively.

Several interesting features are present in the primary amino acid sequence of Hu-Asp2(a) (Figure 2 and SEQ ID No. 4) and Hu-Asp2(b) (Figure 3, SEQ ID No. 6).

Both sequences contain a signal peptide (residues 1-21 in SEQ ID No. 4 and SEQ ID No. 6), a pro-segment, and a catalytic domain containing two copies of the aspartyl protease active site motif (DTG/DSG). The spacing between the first and second active site motifs is variable due to the 25 amino acid residue deletion in Hu-Asp-2(b) 5 and consists of 168-*versus*-194 amino acid residues, for Hu-Asp2(b) and Hu-Asp-2(a), respectively. More interestingly, both sequences contains a predicted transmembrane domain (residues 455-477 in SEQ ID No.4 and 430-452 in SEQ ID No. 6) near their C-termini which indicates that the protease is anchored in the membrane. This feature is not found in any other aspartyl protease except Hu-Asp1.

10

Example 3

Molecular cloning of mouse Asp2 cDNA and genomic DNA.

Cloning and characterization of murine Asp2 cDNA.

The murine ortholog of Hu-Asp2 was cloned using a combination of cDNA 15 library screening, PCR, and genomic cloning. Approximately 500,000 independent clones from a mouse brain cDNA library were screened using a ³²P-labeled coding sequence probe prepared from Hu-Asp2. Replicate positives were subjected to DNA sequence analysis and the longest cDNA contained the entire 3' untranslated region and 47 amino acids in the coding region. PCR amplification of the same mouse brain 20 cDNA library with an antisense oligonucleotide primer specific for the 5'-most cDNA sequence determined above and a sense primer specific for the 5' region of human Asp2 sequence followed by DNA sequence analysis gave an additional 980 bp of the coding sequence. The remainder of the 5' sequence of murine Asp-2 was derived from genomic sequence (see below).

25

Isolation and sequence analysis of the murine Asp-2 gene.

A murine EST sequence encoding a portion of the murine Asp2 cDNA was identified in the GenBank EST database using the BLAST search tool and the 30 Hu-Asp2 coding sequence as the query. Clone g3160898 displayed 88% shared identity to the human sequence over 352 bp. Oligonucleotide primer pairs specific for

this region of murine Asp2 were then synthesized and used to amplify regions of the murine gene. Murine genomic DNA, derived from strain 129/SvJ, was amplified in the PCR (25 cycles) using various primer sets specific for murine Asp2 and the products analyzed by agarose gel electrophoresis. The primer set Zoo-1 and Zoo-4
5 amplified a 750 bp fragment that contained approximately 600 bp of intron sequence based on comparison to the known cDNA sequence. This primer set was then used to screen a murine BAC library by PCR, a single genomic clone was isolated and this cloned was confirmed contain the murine Asp2 gene by DNA sequence analysis.
Shotgun DNA sequencing of this Asp2 genomic clone and comparison to the cDNA
10 sequences of both Hu-Asp2 and the partial murine cDNA sequences defined the full-length sequence of murine Asp2 (SEQ ID No. 7). The predicted amino acid sequence of murine Asp2 (SEQ ID No. 8) showed 96.4% shared identity (GCG BestFit algorithm) with 18/501 amino acid residue substitutions compared to the human sequence (Figure 4). The proteolytic processing of murine Asp2(a) is believed
15 to be analogous to the processing described above for human Asp2(a). In addition, a variant lacking amino acid residues 190-214 of SEQ ID NO: 8 is specifically contemplated as a murine Asp2(b) polypeptide. All forms of murine Asp2(b) gene and protein are intended as aspects of the invention.

20

Example 4

Tissue Distribution of Expression of Hu-Asp2 Transcripts

Materials and Methods:

The tissue distribution of expression of Hu-Asp-2 was determined using multiple tissue Northern blots obtained from Clontech (Palo Alto, CA). Incyte clone
25 2696295 in the vector pINCY was digested to completion with *EcoRI/NotI* and the 1.8 kb cDNA insert purified by preparative agarose gel electrophoresis. This fragment was radiolabeled to a specific activity $> 1 \times 10^9$ dpm/ μ g by random priming in the presence of [α -³²P-dATP] (>3000 Ci/mmol, Amersham, Arlington Heights, IL) and Klenow fragment of DNA polymerase I. Nylon filters containing denatured, size
30 fractionated poly A⁺ RNAs isolated from different human tissues were hybridized

with 2×10^6 dpm/ml probe in ExpressHyb buffer (Clontech, Palo Alto, CA) for 1 hour at 68 °C and washed as recommended by the manufacturer. Hybridization signals were visualized by autoradiography using BioMax XR film (Kodak, Rochester, NY) with intensifying screens at -80 °C.

5

Results and Discussion:

Limited information on the tissue distribution of expression of Hu-Asp-2 transcripts was obtained from database analysis due to the relatively small number of ESTs detected using the methods described above (< 5). In an effort to gain further 10 information on the expression of the Hu-Asp2 gene, Northern analysis was employed to determine both the size(s) and abundance of Hu-Asp2 transcripts. PolyA⁺ RNAs isolated from a series of peripheral tissues and brain regions were displayed on a solid support following separation under denaturing conditions and Hu-Asp2 transcripts were visualized by high stringency hybridization to radiolabeled insert from clone 15 2696295. The 2696295 cDNA probe visualized a constellation of transcripts that migrated with apparent sizes of 3.0kb, 4.4 kb and 8.0 kb with the latter two transcript being the most abundant.

Across the tissues surveyed, Hu-Asp2 transcripts were most abundant in pancreas and brain with lower but detectable levels observed in all other tissues 20 examined except thymus and PBLs. Given the relative abundance of Hu-Asp2 transcripts in brain, the regional expression in brain regions was also established. A similar constellation of transcript sizes were detected in all brain regions examined [cerebellum, cerebral cortex, occipital pole, frontal lobe, temporal lobe and putamen] with the highest abundance in the medulla and spinal cord.

25

Example 5

**Northern Blot Detection of HuAsp-1 and
HuAsp-2 Transcripts in Human Cell Lines**

A variety of human cell lines were tested for their ability to produce Hu-Asp1 30 and Asp2 mRNA. Human embryonic kidney (HEK-293) cells, African green monkey (Cos-7) cells, Chinese hamster ovary (CHO) cells, HELA cells, and the

neuroblastoma cell line IMR-32 were all obtained from the ATCC. Cells were cultured in DME containing 10% FCS except CHO cells which were maintained in α-MEM/10% FCS at 37 °C in 5% CO₂ until they were near confluence. Washed monolayers of cells (3 X 10⁷) were lysed on the dishes and poly A⁺ RNA extracted 5 using the Qiagen Oligotex Direct mRNA kit. Samples containing 2 µg of poly A⁺ RNA from each cell line were fractionated under denaturing conditions (glyoxal-treated), transferred to a solid nylon membrane support by capillary action, and transcripts visualized by hybridization with random-primed labeled (³²P) coding sequence probes derived from either Hu-Asp1 or Hu-Asp2. Radioactive signals were 10 detected by exposure to X-ray film and by image analysis with a PhosphorImager.

The Hu-Asp1 cDNA probe visualized a similar constellation of transcripts (2.6 kb and 3.5 kb) that were previously detected in human tissues. The relative abundance determined by quantification of the radioactive signal was Cos-7 > HEK 292 = HELA > IMR32.

15 The Hu-Asp2 cDNA probe also visualized a similar constellation of transcripts compared to tissue (3.0 kb, 4.4 kb, and 8.0 kb) with the following relative abundance; HEK 293 > Cos 7 > IMR32 > HELA.

Example 6

20 **Modification of APP to increase Aβ processing for in vitro screening**

Human cell lines that process Aβ peptide from APP provide a means to screen in cellular assays for inhibitors of β- and γ-secretase. Production and release of Aβ peptide into the culture supernatant is monitored by an enzyme-linked immunosorbent assay (ELA). Although expression of APP is widespread and both neural and 25 non-neuronal cell lines process and release Aβ peptide, levels of endogenous APP processing are low and difficult to detect by ELA. Aβ processing can be increased by expressing in transformed cell lines mutations of APP that enhance Aβ processing. We made the serendipitous observation that addition of two lysine residues to the carboxyl terminus of APP695 increases Aβ processing still further. This allowed us

to create a transformed cell line that releases A β peptide into the culture medium at the remarkable level of 20,000 pg/ml.

Materials And Methods

Materials:

5 Human embryonic kidney cell line 293 (HEK293 cells) were obtained internally. The vector pIRES-EGFP was purchased from Clontech. Oligonucleotides for mutation using the polymerase chain reaction (PCR) were purchased from Genosys. A plasmid containing human APP695 (SEQ ID No. 9 [nucleotide] and SEQ ID No. 10 [amino acid]) was obtained from Northwestern University Medical School.
10 This was subcloned into pSK (Stratagene) at the *Not*1 site creating the plasmid pAPP695.

Mutagenesis protocol:

The Swedish mutation (K670N, M671L) was introduced into pAPP695 using the Stratagene Quick Change Mutagenesis Kit to create the plasmid pAPP695NL (SEQ ID No. 11 [nucleotide] and SEQ ID No. 12 [amino acid]). To introduce a di-lysine motif at the C-terminus of APP695, the forward primer #276 5'
15 GACTGACCACTCGACCAGGTTC (SEQ ID No. 47) was used with the "patch" primer #274 5'
di-lysine motif at the C-terminus of APP695, the forward primer #276 5'
GAATTAATTCCAGCACACTGGCTACTTCTGTCATCTCAAAGAAC
20 (SEQ ID No. 48) and the flanking primer #275
CGAATTAATTCCAGCACACTGGCTA (SEQ ID No. 49) to modify the 3' end of the APP695 cDNA (SEQ ID No. 15 [nucleotide] and SEQ ID No. 16 [amino acid]). This also added a BstX1 restriction site that will be compatible with the BstX1 site in the multiple cloning site of pIRES-EGFP. PCR amplification was performed with a
25 Clontech HF Advantage cDNA PCR kit using the polymerase mix and buffers supplied by the manufacturer. For "patch" PCR, the patch primer was used at 1/20th the molar concentration of the flanking primers. PCR amplification products were purified using a QIAquick PCR purification kit (Qiagen). After digestion with restriction enzymes, products were separated on 0.8% agarose gels and then excised
30 DNA fragments were purified using a QIAquick gel extraction kit (Qiagen).

To reassemble a modified APP695-Sw cDNA, the 5' Not1-Bgl2 fragment of the APP695-Sw cDNA and the 3' Bgl2-BstX1 APP695 cDNA fragment obtained by PCR were ligated into pIRES-EGFP plasmid DNA opened at the Not1 and BstX1 sites. Ligations were performed for 5 minutes at room temperature using a Rapid 5 DNA Ligation kit (Boehringer Mannheim) and transformed into Library Efficiency DH5a Competent Cells (GibcoBRL Life Technologies). Bacterial colonies were screened for inserts by PCR amplification using primers #276 and #275. Plasmid DNA was purified for mammalian cell transfection using a QIAprep Spin Miniprep kit (Qiagen). The construct obtained was designated pMG125.3 (APPSW-KK, SEQ 10 ID No. 17 [nucleotide] and SEQ ID No. 18 [amino acid]).

Mammalian Cell Transfection:

HEK293 cells for transfection were grown to 80% confluence in Dulbecco's modified Eagle's medium (DMEM) with 10% fetal bovine serum. Cotransfections were performed using LipofectAmine (Gibco-BRL) with 3 µg pMG125.3 DNA and 9 15 µg pcDNA3.1 DNA per 10 x 10⁶ cells. Three days posttransfection, cells were passaged into medium containing G418 at a concentration of 400 µg/ml. After three days growth in selective medium, cells were sorted by their fluorescence.

Clonal Selection of 125.3 cells by FACS:

Cell samples were analyzed on an EPICS Elite ESP flow cytometer (Coulter, 20 Hialeah, FL) equipped with a 488 nm excitation line supplied by an air-cooled argon laser. EGFP emission was measured through a 525 nm band-pass filter and fluorescence intensity was displayed on a 4-decade log scale after gating on viable cells as determined by forward and right angle light scatter. Single green cells were separated into each well of one 96 well plate containing growth medium without 25 G418. After a four day recovery period, G418 was added to the medium to a final concentration of 400 µg/ml. After selection, 32% of the wells contained expanding clones. Wells with clones were expanded from the 96 well plate to a 24 well plate and then a 6 well plate with the fastest growing colonies chosen for expansion at each passage. The final cell line selected was the fastest growing of the final six passaged. 30 This clone, designated 125.3, has been maintained in G418 at 400 ug/ml with passage

every four days into fresh medium. No loss of A β production of EGFP fluorescence has been seen over 23 passages.

A β EIA Analysis (Double Antibody Sandwich ELISA for hA β 1-40/42):

Cell culture supernatants harvested 48 hours after transfection were analyzed
5 in a standard A β EIA as follows. Human A β 1-40 or 1-42 was measured using monoclonal antibody (mAb) 6E10 (Senetek, St. Louis, MO) and biotinylated rabbit antiserum 162 or 164 (New York State Institute for Basic Research, Staten Island, NY) in a double antibody sandwich ELISA. The capture antibody 6E10 is specific to an epitope present on the N-terminal amino acid residues 1-16 of hA β . The
10 conjugated detecting antibodies 162 and 164 are specific for hA β 1-40 and 1-42, respectively. Briefly, a Nunc Maxisorp 96 well immunoplate was coated with 100 μ l/well of mAb 6E10 (5 μ g/ml) diluted in 0.1M carbonate-bicarbonate buffer, pH 9.6 and incubated at 4°C overnight. After washing the plate 3x with 0.01M DPBS
15 (Modified Dulbecco's Phosphate Buffered Saline (0.008M sodium phosphate, 0.002M potassium phosphate, 0.14M sodium chloride, 0.01 M potassium chloride, pH 7.4) from Pierce, Rockford, IL) containing 0.05% of Tween-20 (DPBST), the plate was blocked for 60 minutes with 200 μ l of 10% normal sheep serum (Sigma) in 0.01M DPBS to avoid non-specific binding. Human A β 1-40 or 1-42 standards 100 μ l/well
20 (Bachem, Torrance, CA) diluted, from a 1mg/ml stock solution in DMSO, in culture medium was added after washing the plate, as well as 100 μ l/well of sample, e.g., conditioned medium of transfected cells.

The plate was incubated for 2 hours at room temperature and 4°C overnight. The next day, after washing the plate, 100 μ l/well biotinylated rabbit antiserum 162 1:400 or 164 1:50 diluted in DPBST + 0.5% BSA was added and incubated at room
25 temperature for 1 hour, 15 minutes. Following washes, 100 μ l/well neutravidin-horseradish peroxidase (Pierce, Rockford, IL) diluted 1:10,000 in DPBST was applied and incubated for 1 hour at room temperature. After the last washes 100 μ l/well of o-phenylenediamine dihydrochloride (Sigma Chemicals, St. Louis, MO) in 50mM citric acid/100mM sodium phosphate buffer (Sigma Chemicals, St. Louis,
30 MO), pH 5.0, was added as substrate and the color development was monitored at

450nm in a kinetic microplate reader for 20 minutes using Soft max Pro software. All standards and samples were run in triplicates. The samples with absorbance values falling within the standard curve were extrapolated from the standard curves using Soft max Pro software and expressed in pg/ml culture medium.

5 *Results:*

Addition of two lysine residues to the carboxyl terminus of APP695 greatly increases A β processing in HEK293 cells as shown by transient expression (Table 1). Addition of the di-lysine motif to APP695 increases A β processing to that seen with the APP695 containing the Swedish mutation. Combining the di-lysine motif with the 10 Swedish mutation further increases processing by an additional 2.8 fold.

Cotransformation of HEK293 cells with pMG125.3 and pcDNA3.1 allowed dual selection of transformed cells for G418 resistance and high level expression of EGFP. After clonal selection by FACS, the cell line obtained, produces a remarkable 20,000 pg A β peptide per ml of culture medium after growth for 36 hours in 24 well 15 plates. Production of A β peptide under various growth conditions is summarized in Table 2.

20

25

30

TABLE 1

Release of A β peptide into the culture medium 48 hours after transient transfection of HEK293 cells with the indicated vectors containing wildtype or modified APP. Values tabulated are mean + SD and P-value for pairwise comparison using Student's t-test assuming unequal variances.

	APP Construct	A β 1-40 peptide (pg/ml)	Fold Increase	P-value
10	pIRES-EGFP vector	147 + 28	1.0	
15	wt APP695 (142.3)	194 + 15	1.3	0.051
	wt APP695-KK (124.1)	424 + 34	2.8	3 x 10 ⁻⁵
	APP695-Sw (143.3)	457 + 65	3.1	2 x 10 ⁻³
20	APP695-SwKK (125.3)	1308 + 98	8.9	3 x 10 ⁻⁴

TABLE 2
Release of A β peptide from HEK125.3 cells under various growth conditions.

5	Type of Culture	Volume of Medium	Duration of Culture	A β 1-40 (pg/ml)	A β 1-42 (pg/ml)
10	Plate				
	24 well plate	400 ul	36 hr	28,036	1,439

Example 7

Antisense oligomer inhibition of Abeta processing in HEK125.3 cells

15 The sequences of Hu-Asp1 and Hu-Asp2 were provided to Sequitur, Inc (Natick, MA) for selection of targeted sequences and design of 2nd generation chimeric antisense oligomers using proprietary technology (Sequitur Ver. D Pat pending #3002). Antisense oligomers Lot# S644, S645, S646 and S647 were targeted against Asp1. Antisense oligomers Lot# S648, S649, S650 and S651 were targeted
 20 against Asp2. Control antisense oligomers Lot# S652, S653, S655, and S674 were targeted against an irrelevant gene and antisense oligomers Lot #S656, S657, S658, and S659 were targeted against a second irrelevant gene.

25 For transfection with the antisense oligomers, HEK125.3 cells were grown to about 50% confluence in 6 well plates in Minimal Essential Medium (MEM) supplemented with 10% fetal calf serum. A stock solution of oligofectin G (Siquitur Inc., Natick, MA) at 2 mg/ml was diluted to 50 μ g/ml in serum free MEM. Separately, the antisense oligomer stock solution at 100 μ M was diluted to 800 nM in Opti-MEM (GIBCO-BRL, Grand Island, NY). The diluted stocks of oligofectin G and antisense oligomer were then mixed at a ratio of 1:1 and incubated at room
 30 temperature. After 15 minutes incubation, the reagent was diluted 10 fold into MEM

containing 10% fetal calf serum and 2 ml was added to each well of the 6 well plate after first removing the old medium. After transfection, cells were grown in the continual presence of the oligofectin G/antisense oligomer. To monitor A β peptide release, 400 μ l of conditioned medium was removed periodically from the culture well and replaced with fresh medium beginning 24 hours after transfection. A β peptides in the conditioned medium were assayed via immunoprecipitation and Western blotting. Data reported are from culture supernatants harvested 48 hours after transfection.

The 16 different antisense oligomers obtained from Sequitur Inc. were transfected separately into HEK125.3 cells to determine their affect on A β peptide processing. Only antisense oligomers targeted against Asp2 significantly reduced Abeta processing by HEK125.3 cells. Both A β (1-40) and A β (1-42) were inhibited by the same degree. In Table 3, percent inhibition is calculated with respect to untransfected cells. Antisense oligomer reagents giving greater than 50% inhibition are marked with an asterisk. For ASP2, 4 of 4 antisense oligomers gave greater than 50% inhibition with an average inhibition of 62% for A β 1-40 processing and 60% for A β 1-42 processing.

TABLE 3
Inhibition of A β peptide release from HEK125.3 cells treated with antisense oligomers.

	Gene Targeted	Antisense Oligomer	Abeta (1-40)	Abeta (1-42)
5	Asp2-1	S648	71%*	67%*
	Asp2-2	S649	83%*	76%*
	Asp2-3	S650	46%*	50%*
	Asp2-4	S651	47%*	46%*
10	Con1-1	S652	13%	18%
	Con1-2	S653	35%	30%
	Con1-3	S655	9%	18%
	Con1-4	S674	29%	18%
15	Con2-1	S656	12%	18%
	Con2-2	S657	16%	19%
	Con2-3	S658	8%	35%
	Con2-4	S659	3%	18%
20				
25				
30				

Since HEK293 cells derive from kidney, the experiment was extended to human IMR-32 neuroblastoma cells which express all three APP isoforms and which release A β peptides into conditioned medium at measurable levels. [See Neill *et al.*,

J. NeuroSci. Res., (1994) 39: 482-93; and Asami-Odaka *et al.*, *Biochem.*, (1995) 34:10272-8.] Essentially identical results were obtained in the neuroblastoma cells as the HEK293 cells. As shown in Table 3B, the pair of Asp2 antisense oligomers reduced Asp2 mRNA by roughly one-half, while the pair of reverse control oligomers lacked this effect (Table 3B).

Table 3B

Reduction of A β 40 and A β 42 in human neuroblastoma IMR-32 cells and mouse neuroblastoma Neuro-2A cells treated with Asp2 antisense and control oligomers as indicated. Oligomers were transfected in quadruplicate cultures. Values tabulated are normalized against cultures treated with oligofectin-G™ only (mean + SD, ** p<0.001 compared to reverse control oligomer).

	Asp2 mRNA	IMR-32 cells		Neuro-2A cells	
		A β 40	A β 42	A β 40	A β 42
Asp2-1A	-75%	-49 + 2%**	-42 + 14%**	-70 + 7%**	-67 + 2%**
Asp2-1R	0.16	-0 + 3%	21.26	-9 + 15%	1.05
Asp2-2A	-39%	-43 + 3%**	-44 + 18%**	-61 + 12%**	-61 + 12%**
Asp2-2R	0.47	12.2	19.22	6.15	-8 + 10%

20

Together with the reduction in Asp2 mRNA there was a concomitant reduction in the release of A β 40 and A β 42 peptides into the conditioned medium. Thus, Asp2 functions directly or indirectly in a human kidney and a human neuroblastoma cell line to facilitate the processing of APP into A β peptides. Molecular cloning of the mouse Asp2 cDNA revealed a high degree of homology to human (>96% amino acid identity, see Example 3), and indeed, complete nucleotide identity at the sites targeted by the Asp2-1A and Asp2-2A antisense oligomers. Similar results were obtained in mouse Neuro-2a cells engineered to express APP-Sw-KK. The Asp2 antisense

oligomers reduced release of A β peptides into the medium while the reverse control oligomers did not (Table 3B). Thus, the three antisense experiments with HEK293, IMR-32 and Neuro-2a cells indicate that Asp2 acts directly or indirectly to facilitate A β processing in both somatic and neural cell lines.

5

Example 8

Demonstration of Hu-Asp2 β -Secretase Activity in Cultured Cells

Several mutations in APP associated with early onset Alzheimer's disease have been shown to alter A β peptide processing. These flank the - and C-terminal cleavage sites that release A β from APP. These cleavage sites are referred to as the β -secretase and γ -secretase cleavage sites, respectively. Cleavage of APP at the β -secretase site creates a C-terminal fragment of APP containing 99 amino acids of 11,145 daltons molecular weight. The Swedish KM-NL mutation immediately upstream of the β -secretase cleavage site causes a general increase in production of both the 1-40 and 1-42 amino acid forms of A β peptide. The London VF mutation (V717-F in the APP770 isoform) has little effect on total A β peptide production, but appears to preferentially increase the percentage of the longer 1-42 amino acid form of A β peptide by affecting the choice of β -secretase cleavage site used during APP processing. Thus, we sought to determine if these mutations altered the amount and type of A β peptide produced by cultured cells cotransfected with a construct directing expression of Hu-Asp2.

Two experiments were performed which demonstrate Hu-Asp2 β -secretase activity in cultured cells. In the first experiment, treatment of HEK125.3 cells with antisense oligomers directed against Hu-Asp2 transcripts as described in Example 7 was found to decrease the amount of the C-terminal fragment of APP created by β -secretase cleavage (CTF99) (Figure 9). This shows that Hu-Asp2 acts directly or indirectly to facilitate β -secretase cleavage. In the second experiment, increased expression of Hu-Asp2 in transfected mouse Neuro2A cells is shown to increase accumulation of the CTF99 β -secretase cleavage fragment (Figure 10). This increase is seen most easily when a mutant APP-KK clone containing a C-terminal di-lysine

motif is used for transfection. A further increase is seen when Hu-Asp2 is cotransfected with APP-Sw-KK containing the Swedish mutation KM →NL. The Swedish mutation is known to increase cleavage of APP by the β-secretase.

A second set of experiments demonstrate Hu-Asp2 facilitates γ-secretase activity in cotransfection experiments with human embryonic kidney HEK293 cells. 5 Cotransfection of Hu-Asp2 with an APP-KK clone greatly increases production and release of soluble Aβ1-40 and Aβ1-42 peptides from HEK293 cells. There is a proportionately greater increase in the release of Aβ1-42. A further increase in production of Aβ1-42 is seen when Hu-Asp2 is cotransfected with APP-VF (SEQ ID 10 No. 13 [nucleotide] and SEQ ID No. 14 [amino acid]) or APP-VF-KK SEQ ID No. 19 [nucleotide] and SEQ ID No. 20 [amino acid]) clones containing the London mutation V717-F. The V717-F mutation is known to alter cleavage specificity of the APP γ-secretase such that the preference for cleavage at the Aβ42 site is increased. Thus, Asp2 acts directly or indirectly to facilitate γ-secretase processing of APP at the β42 15 cleavage site.

Materials

Antibodies 6E10 and 4G8 were purchased from Senetek (St. Louis, MO). Antibody 369 was obtained from the laboratory of Paul Greengard at the Rockefeller University. Antibody C8 was obtained from the laboratory of Dennis Selkoe at the 20 Harvard Medical School and Brigham and Women's Hospital.

APP Constructs used

The APP constructs used for transfection experiments comprised the following

APP: wild-type APP695 (SEQ ID No. 9 and No. 10)

APP-Sw: APP695 containing the Swedish KM-NL mutation (SEQ ID No. 11 25 and No. 12 , wherein the lysine (K) at residue 595 of APP695 is changed to asparagine (N) and the methionine (M) at residue 596 of APP695 is changed to leucine (L).),

APP-VF: APP695 containing the London V-F mutation (SEQ ID Nos. 13 & 14) (Affected residue 717 of the APP770 isoform corresponds with residue 642 of the

APP695 isoform. Thus, APP-VF as set in SEQ ID NO: 14 comprises the APP695 sequence, wherein the valine (V) at residue 642 is changed to phenylalanine (F).)

APP-KK: APP695 containing a C-terminal KK motif (SEQ ID Nos. 15 & 16),

APP-Sw-KK: APP695-Sw containing a C-terminal KK motif (SEQ ID No. 17
5 & 18),

APP-VF-KK: APP695-VF containing a C-terminal KK motif (SEQ ID Nos.
19 & 20).

These were inserted into the vector pIRES-EGFP (Clontech, Palo Alto CA)
between the *Not*1 and *Bst*X1 sites using appropriate linker sequences introduced by
10 PCR.

*Transfection of antisense oligomers or plasmid DNA constructs in HEK293 cells,
HEK125.3 cells and Neuro-2A cells,*

Human embryonic kidney HEK293 cells and mouse Neuro-2a cells were
15 transfected with expression constructs using the Lipofectamine Plus reagent from
Gibco/BRL. Cells were seeded in 24 well tissue culture plates to a density of 70-80%
confluence. Four wells per plate were transfected with 2 µg DNA (3:1,
APP:cotransfector), 8 µl Plus reagent, and 4 µl Lipofectamine in OptiMEM.
OptiMEM was added to a total volume of 1 ml, distributed 200 µl per well and
20 incubated 3 hours. Care was taken to hold constant the ratios of the two plasmids used
for cotransfection as well as the total amount of DNA used in the transfection. The
transfection media was replaced with DMEM, 10%FBS, NaPyruvate, with
antibiotic/antimycotic and the cells were incubated under normal conditions (37°C,
5% CO₂) for 48 hours. The conditioned media were removed to polypropylene tubes
25 and stored at -80°C until assayed for the content of Aβ1-40 and Aβ1-42 by EIA as
described in the preceding examples. Transfection of antisense oligomers into
HEK125.3 cells was as described in Example 7.

Preparation of cell extracts, Western blot protocol

Cells were harvested after being transfected with plasmid DNA for about 60
30 hours. First, cells were transferred to 15-ml conical tube from the plate and

centrifuged at 1,500 rpm for 5 minutes to remove the medium. The cell pellets were washed once with PBS. We then lysed the cells with lysis buffer (10 mM HEPES, pH 7.9, 150 mM NaCl, 10% glycerol, 1 mM EGTA, 1 mM EDTA, 0.1 mM sodium vanadate and 1% NP-40). The lysed cell mixtures were centrifuged at 5000 rpm and the supernatant was stored at -20°C as the cell extracts. Equal amounts of extracts from HEK125.3 cells transfected with the Asp2 antisense oligomers and controls were precipitated with antibody 369 that recognizes the C-terminus of APP and then CTF99 was detected in the immunoprecipitate with antibody 6E10. The experiment was repeated using C8, a second precipitating antibody that also recognizes the C-terminus of APP. For Western blot of extracts from mouse Neuro-2a cells cotransfected with Hu-Asp2 and APP-KK, APP-Sw-KK, APP-VF-KK or APP-VF, equal amounts of cell extracts were electrophoresed through 4-10% or 10-20% Tricine gradient gels (NOVEX, San Diego, CA). Full length APP and the CTF99 β -secretase product were detected with antibody 6E10.

15 *Results*

Transfection of HEK125.3 cells with Asp2-1 or Asp2-2 antisense oligomers reduces production of the CTF β -secretase product in comparison to cells similarly transfected with control oligomers having the reverse sequence (Asp2-1 reverse & Asp2-2 reverse), see Figure 9. Correspondingly, cotransfection of Hu-Asp2 into mouse Neuro-2a cells with the APP-KK construct increased the formation of CTF99. (See Fig. 10.) This was further increased if Hu-Asp2 was coexpressed with APP-Sw-KK, a mutant form of APP containing the Swedish KM~NL mutation that increases β -secretase processing.

Effects of Asp2 on the production of Ab peptides from endogenously expressed APP isoforms were assessed in HEK293 cells transfected with a construct expressing Asp2 or with the empty vector after selection of transformants with the antibiotic G418. A β 40 production was increased in cells transformed with the Asp2 construct in comparison to those transformed with the empty vector DNA. A β 40 levels in conditioned medium collected from the Asp2 transformed and control cultures was 424 \pm 45 pg /ml and 113 \pm 58 pg/ml, respectively (p<0.001). A β 42

release was below the limit of detection by the EIA, while the release of sAPP α was unaffected, 112 ± 8 ng/ml versus 111 ± 40 ng/ml. This further indicates that Asp2 acts directly or indirectly to facilitate the processing and release of A β from endogenously expressed APP.

5 Co-transfection of Hu-Asp2 with APP has little effect on A β 40 production but increases A β 42 production above background (Table 4). Addition of the di-lysine motif to the C-terminus of APP increases A β peptide processing about two fold, although A β 40 and A β 42 production remain quite low (352 pg/ml and 21 pg/ml, respectively). Cotransfection of Asp2 with APP-KK further increases both A β 40 and
10 A β 42 production.

The APP V717-F mutation has been shown to increase γ -secretase processing at the A β 42 cleavage site. Cotransfection of Hu-Asp2 with the APP-VF or APP-VF-KK constructs increased A β 42 production (a two fold increase with APP-VF and a four-fold increase with APP-VF-KK, Table 4), but had mixed effects on A β 40 production (a slight decrease with APP-VF, and a two fold increase with APP-VF-KK in comparison to the pcDNA cotransfection control. Thus, the effect of Asp2 on A β 42 production was proportionately greater leading to an increase in the ratio of A β 42/total Ab. Indeed, the ratio of A β 42/total A β reaches a very high value of 42% in HEK293 cells cotransfected with Hu-Asp2 and APP-VF-KK.
15
20

25

30

Table 4

Results of cotransfected Hu-Asp2 or pcDNA plasmid DNA with various APP constructs containing the V717-F mutation that modifies γ -secretase processing.

5 Cotransfection with Asp2 consistently increases the ratio of A β 42/total A β . Values
tabulated are A β peptide pg/ml.

	pcDNA Cotransfection			Asp2 Cotransfection		
	A β 40	A β 42	A β 42/Tot	A β 40	A β 42	A β 42/Tot
10			al			al
	APP	192 \pm 1	<4	<2%	188 \pm 40	8 \pm 10
		8				
	APP-VF	118 \pm 1	15 \pm 19	11.5%	85 \pm 7	24 \pm 12
		5				
15	APP-KK	352 \pm 2	21 \pm 6	5.5%	1062 \pm 101	226 \pm 4
		4				9
	APP-VF-K	230 \pm 3	88 \pm 24	27.7%	491 \pm 35	355 \pm 3
	K	1				6
20						

Example 9**Bacterial expression of human Asp2(a)***Expression of recombinant Hu-Asp2(a) in E. coli.*

Hu-Asp2(a) can be expressed in *E. coli* after addition of N-terminal sequences
5 such as a T7 tag (SEQ ID No. 21 and No. 22) or a T7 tag followed by a caspase 8
leader sequence (SEQ ID No. 23 and No. 24). Alternatively, reduction of the GC
content of the 5' sequence by site directed mutagenesis can be used to increase the
yield of Hu-Asp2 (SEQ ID No. 25 and No. 26). In addition, Asp2(a) can be
engineered with a proteolytic cleavage site (SEQ ID No. 27 and No. 28). To produce
10 a soluble protein after expression and refolding, deletion of the transmembrane
domain and cytoplasmic tail, or deletion of the membrane proximal region,
transmembrane domain, and cytoplasmic tail is preferred. Any materials (vectors,
host cells, etc.) and methods described herein to express Hu-Asp2(a) should in
principle be equally effective for expression of Hu-Asp2(b).

15 Methods

PCR with primers containing appropriate linker sequences was used to
assemble fusions of Asp2(a) coding sequence with N-terminal sequence modifications
including a T7 tag (SEQ ID Nos. 21 and 22) or a T7-caspase 8 leader (SEQ ID Nos.
23 and 24). These constructs were cloned into the expression vector pet23a(+)
20 [Novagen] in which a T7 promoter directs expression of a T7 tag preceding a
sequence of multiple cloning sites. To clone Hu-Asp2 sequences behind the T7 leader
of pet23a(+), the following oligonucleotides were used for amplification of the selected
Hu-Asp2(a) sequence: #553=GTGGATCCACCCAGCACGGCATCCGGCTG (SEQ
ID No. 35), #554=GAAAGCTTCATGACTCATCTGTCTGTGGAATGTTG (SEQ
25 ID No. 36) which placed BamHI and HindIII sites flanking the 5' and 3' ends of the
insert, respectively. The Asp2(a) sequence was amplified from the full length Asp2(a)
cDNA cloned into pcDNA3.1 using the Advantage-GC cDNA PCR [Clontech]
following the manufacturer's supplied protocol using annealing & extension at 68°C in
a two-step PCR cycle for 25 cycles. The insert and vector were cut with BamHI and
30 HindIII, purified by electrophoresis through an agarose gel, then ligated using the

Rapid DNA Ligation kit [Boehringer Mannheim]. The ligation reaction was used to transform the *E. coli* strain JM109 (Promega) and colonies were picked for the purification of plasmid (Qiagen,Qiaprep minispin) and DNA sequence analysis . For inducible expression using induction with isopropyl b-D-thiogalactopyranoside (IPTG), the expression vector was transferred into *E. coli* strain BL21 (Statagene).
5 Bacterial cultures were grown in LB broth in the presence of ampicillin at 100 ug/ml, and induced in log phase growth at an OD600 of 0.6-1.0 with 1 mM IPTG for 4 hour at 37°C. The cell pellet was harvested by centrifugation.

To clone Hu-Asp2 sequences behind the T7 tag and caspase leader (SEQ ID
10 Nos. 23 and 24), the construct created above containing the T7-Hu-Asp2 sequence (SEQ ID Nos. 21 and 22) was opened at the BamH1 site, and then the phosphorylated caspase 8 leader oligonucleotides
#559=GATCGATGACTATCTCTGACTCTCCGCGTGAACAGGGACG (SEQ ID No. 37), #560=GATCCGTCTGTTCACGCGGAGAGTCAGAGATAGTCATC (SEQ
15 ID No. 38) were annealed and ligated to the vector DNA. The 5' overhang for each set of oligonucleotides was designed such that it allowed ligation into the BamHI site but not subsequent digestion with BamHI. The ligation reaction was transformed into JM109 as above for analysis of protein expression after transfer to *E. coli* strain BL21.

In order to reduce the GC content of the 5' terminus of asp2(a), a pair of
20 antiparallel oligos were designed to change degenerate codon bases in 15 amino acid positions from G/C to A/T (SEQ ID Nos. 25 and 26). The new nucleotide sequence at the 5' end of asp2 did not change the encoded amino acid and was chosen to optimize *E. Coli* expression. The sequence of the sense linker is 5'
CGGCATCCGGCTGCCCTGCGTAGCGGTCTGGGTGGTGCTCCACTGGGTCT
25 GCGTCTGCCCGGGAGACCGACGAA G 3' (SEQ ID No. 39). The sequence of the antisense linker is : 5'
CTTCGTCGGTCTCCGGGGCAGACGCAGACCCAGTGGAGCACCACCCAGA
CCGCTACGCAGGGGCAGCCGGATGCCG 3' (SEQ ID No. 40). After annealing the phosphorylated linkers together in 0.1 M NaCl-10 mM Tris, pH 7.4 they were
30 ligated into unique Cla I and Sma I sites in Hu-Asp2 in the vector pTAC. For

inducible expression using induction with isopropyl b-D-thiogalactopyranoside (IPTG), bacterial cultures were grown in LB broth in the presence of ampicillin at 100 ug/ml, and induced in log phase growth at an OD600 of 0.6-1.0 with 1 mM IPTG for 4 hour at 37°C. The cell pellet was harvested by centrifugation.

5 To create a vector in which the leader sequences can be removed by limited proteolysis with caspase 8 such that this liberates a Hu-Asp2 polypeptide beginning with the N-terminal sequence GSFV (SEQ ID Nos. 27 and 28), the following procedure was followed. Two phosphorylated oligonucleotides containing the caspase 8 cleavage site IETD, #571=5'

10 GATCGATGACTATCTCTGACTCTCCGCTGGACTCTGGTATCGAAACCGACG (SEQ ID No. 41) and #572= GATCCGTCGGTTTCGATACCAGAGTCCAGCGGAGAGTCAGAGATAGTCAT C (SEQ ID No. 42) were annealed and ligated into pET23a+ that had been opened with BamHI. After transformation into JM109, the purified vector DNA was

15 recovered and orientation of the insert was confirmed by DNA sequence analysis.

The following oligonucleotides were used for amplification of the selected Hu-Asp2(a) sequence: #573=5'AAGGATCCTTGTGGAGATGGTGGACAACCTG, (SEQ ID No. 43) #554=GAAAGCTTCATGACTCATCTGTCTGTGGAATGTTG (SEQ ID No. 44) which placed BamHI and HindIII sites flanking the 5' and 3' ends of the insert, respectively. The Hu-Asp2(a) sequence was amplified from the full length Hu-Asp2(a) cDNA cloned into pcDNA3.1 using the Advantage-GC cDNA PCR [Clontech] following the manufacturer's supplied protocol using annealing & extension at 68°C in a two-step PCR cycle for 25 cycles. The insert and vector were cut with BamHI and HindIII, purified by electrophoresis through an agarose gel, then ligated using the Rapid DNA Ligation kit [Boehringer Mannheim]. The ligation reaction was used to transform the *E. coli* strain JM109 [Promega] and colonies were picked for the purification of plasmid (Qiagen,Qiaprep minispin) and DNA sequence analysis . For inducible expression using induction with isopropyl b-D-thiogalactopyranoside (IPTG), the expression vector was transferred into *E. coli* strain BL21 (Statagene). Bacterial cultures were grown in LB broth in the presence of

ampicillin at 100 ug/ml, and induced in log phase growth at an OD600 of 0.6-1.0 with 1 mM IPTG for 4 hour at 37°C. The cell pellet was harvested by centrifugation.

To assist purification, a 6-His tag can be introduced into any of the above constructs following the T7 leader by opening the construct at the BamHI site and then ligating in the annealed, phosphorylated oligonucleotides containing the six histidine sequence #565=GATCGCATCATCACCATCACCATG (SEQ ID No. 45), #566=GATCCATGGTGTGGTGATGATGC (SEQ ID No. 46). The 5' overhang for each set of oligonucleotides was designed such that it allowed ligation into the BamHI site but not subsequent digestion with BamHI.

10 *Preparation of Bacterial Pellet:*

36.34g of bacterial pellet representing 10.8L of growth was dispersed into a total volume of 200ml using a 20mm tissue homogenizer probe at 3000 to 5000 rpm in 2M KCl, 0.1M Tris, 0.05M EDTA, 1mM DTT. The conductivity adjusted to about 193mMhos with water. After the pellet was dispersed, an additional amount of the KCl solution was added, bringing the total volume to 500 ml. This suspension was homogenized further for about 3 minutes at 5000 rpm using the same probe. The mixture was then passed through a Rannie high-pressure homogenizer at 10,000psi.

In all cases, the pellet material was carried forward, while the soluble fraction was discarded. The resultant solution was centrifuged in a GSA rotor for 1 hour at 12,500 rpm. The pellet was resuspended in the same solution (without the DTT) using the same tissue homogenizer probe at 2,000 rpm. After homogenizing for 5 minutes at 3000 rpm, the volume was adjusted to 500ml with the same solution, and spun for 1 hour at 12,500 rpm. The pellet was then resuspended as before, but this time the final volume was adjusted to 1.5L with the same solution prior to homogenizing for 5 minutes. After centrifuging at the same speed for 30 minutes, this procedure was repeated. The pellet was then resuspended into about 150ml of cold water, pooling the pellets from the six centrifuge tubes used in the GSA rotor. The pellet has homogenized for 5 minutes at 3,000 rpm, volume adjusted to 250ml with cold water, then spun for 30 minutes. Weight of the resultant pellet was 17.75g.

Summary: Lysis of bacterial pellet in KCl solution, followed by centrifugation in a GSA rotor was used to initially prepare the pellet. The same solution was then used an additional three times for resuspension/homogenization. A final water wash/homogenization was then performed to remove excess KCl and EDTA.

5 *Solublization of Recombinant Hu-Asp2(a):*

A ratio of 9-10ml/gram of pellet was utilized for solubilizing the rHuAsp2L from the pellet previously described. 17.75g of pellet was thawed, and 150ml of 8M guanidine HCl, 5mM β ME, 0.1% DEA, was added. 3M Tris was used to titrate the pH to 8.6. The pellet was initially resuspended into the guanidine solution using a 20 mm tissue 10 homogenizer probe at 1000 rpm. The mixture was then stirred at 4°C for 1 hour prior to centrifugation at 12,500 rpm for 1 hour in GSA rotor. The resultant supernatant was then centrifuged for 30 minutes at 40,000 x g in an SS-34 rotor. The final supernatant was then stored at -20°C, except for 50 ml.

15 *Immobilized Nickel Affinity Chromatography of Solubilized Recombinant Hu-Asp2(a):*

The following solutions were utilized:

- A) 6M Guanidine HCl, 0.1M NaP, pH 8.0, 0.01M Tris, 5mM β ME, 0.5mM Imidazole
- 20 A') 6M Urea, 20mM NaP, pH 6.80, 50mM NaCl
- B') 6M Urea, 20mM NaP, pH 6.20, 50mM NaCl, 12mM Imidazole
- C') 6M Urea, 20mM NaP, pH 6.80, 50mM NaCl, 300mM Imidazole

Note: Buffers A' and C' were mixed at the appropriate ratios to give intermediate concentrations of Imidazole.

25 The 50ml of solubilized material was combined with 50ml of buffer A prior to adding to 100-125ml Qiagen Ni-NTA SuperFlow (pre-equilibrated with buffer A) in a 5 x 10cm Bio-Rad econo column. This was shaken gently overnight at 4°C in the cold room.

Chromatography Steps:

30 Drained the resultant flow through.

Washed with 50ml buffer A (collecting into flow through fraction)

Washed with 250ml buffer A (wash 1)

Washed with 250ml buffer A (wash 2)
Washed with 250ml buffer A'
Washed with 250ml buffer B'
Washed with 250ml buffer A'

5 Eluted with 250ml 75mM Imidazole
Eluted with 250ml 150mM Imidazole (150-1)
Eluted with 250ml 150mM Imidazole (150-2)
Eluted with 250ml 300mM Imidazole (300-1)
Eluted with 250ml 300mM Imidazole (300-2)

10 Eluted with 250ml 300mM Imidazole (300-3)

Chromatography Results:

The Hu-Asp(a) eluted at 75mM Imidazole through 300mM Imidazole. The 75mM fraction, as well as the first 150mM Imidazole (150-1) fraction contained 15 contaminating proteins as visualized on Coomassie Blue stained gels. Therefore, fractions 150-2 and 300-1 will be utilized for refolding experiments since they contained the greatest amount of protein as visualized on a Coomassie Blue stained gel.

Refolding Experiments of Recombinant Hu-Asp2(a):

20 Experiment 1:
Forty ml of 150-2 was spiked with 1M DTT, 3M Tris, pH 7.4 and DEA to a final concentration of 6mM, 50mM, and 0.1% respectively. This was diluted suddenly (while stirring) with 200ml of (4°C) cold 20mM NaP, pH 6.8, 150mM NaCl. This dilution gave a final Urea concentration of 1M. This solution remained clear, even if 25 allowed to set open to the air at room temperature (RT) or at 4°C .
After setting open to the air for 4-5 hours at 4°C, this solution was then dialyzed overnight against 20mM NaP, pH 7.4, 150mM NaCl, 20% glycerol. This method effectively removes the urea in the solution without precipitation of the protein.

Experiment 2:

Some of the 150-2 eluate was concentrated 2x on an Amicon Centriprep, 10,000 MWCO, then treated as in Experiment 1. This material also stayed in solution, with no visible precipitation.

5 *Experiment 3:*

89ml of the 150-2 eluate was spiked with 1M DTT, 3M Tris, pH 7.4 and DEA to a final concentration of 6mM, 50mM, and 0.1% respectively. This was diluted suddenly (while stirring) with 445ml of (4°C) cold 20mM NaP, pH 6.8, 150mM NaCl. This solution appeared clear, with no apparent precipitation. The solution was 10 removed to RT and stirred for 10 minutes prior to adding MEA to a final concentration of 0.1mM. This was stirred slowly at RT for 1 hour. Cystamine and CuSO₄ were then added to final concentrations of 1mM and 10 µM respectively. The solution was stirred slowly at RT for 10 minutes prior to being moved to the 4°C cold room and shaken slowly overnight, open to the air.

15 The following day, the solution (still clear, with no apparent precipitation) was centrifuged at 100,000 x g for 1 hour. Supernatants from multiple runs were pooled, and the bulk of the stabilized protein was dialyzed against 20mM NaP, pH 7.4, 150mM NaCl, 20% glycerol. After dialysis, the material was stored at -20°C.

20 Some (about 10 ml) of the protein solution (still in 1M Urea) was saved back for biochemical analyses, and frozen at -20°C for storage.

Example 10

Expression of Hu-Asp2 and Derivatives in Insect Cells

Any materials (vectors, host cells, etc.) and methods that are useful to express 25 Hu-Asp2(a) should in principle be equally effective for expression of Hu-Asp2(b).

Expression by baculovirus infection.

The coding sequence of Hu-Asp2(a) and Hu-ASp2(b) and several derivatives were engineered for expression in insect cells using the PCR. For the full-length sequence, a 5'-sense oligonucleotide primer that modified the translation initiation site 30 to fit the Kozak consensus sequence was paired with a 3'-antisense primer that

contains the natural translation termination codon in the Hu-Asp2 sequence. PCR amplification of the pcDNA3.1(hygro)/Hu-Asp2(a) template was used to prepare two derivatives of Hu-Asp2(a) or Hu-Asp(b) that delete the C-terminal transmembrane domain (SEQ ID Nos. 29-30 and 50-51, respectively) or delete the transmembrane 5 domain and introduce a hexa-histidine tag at the C-terminus (SEQ ID Nos. 31-32 and 52-53) respectively, were also engineered using PCR. The same 5'-sense oligonucleotide primer described above was paired with either a 3'-antisense primer that (1) introduced a translation termination codon after codon 453 (SEQ ID No. 3) or (2) incorporated a hexa-histidine tag followed by a translation termination codon in 10 the PCR using pcDNA3.1(hygro)/Hu-Asp-2(a) as the template. In all cases, the PCR reactions were performed amplified for 15 cycles using *Pwo*I DNA polymerase (Boehringer-Mannheim) as outlined by the supplier. The reaction products were digested to completion with *Bam*H I and *Not*I and ligated to *Bam*H I and *Not*I digested 15 baculovirus transfer vector pVL1393 (Invitrogen). A portion of the ligations was used to transform competent *E. coli* DH5₋ cells followed by antibiotic selection on LB-Amp. Plasmid DNA was prepared by standard alkaline lysis and banding in CsCl to yield the baculovirus transfer vectors pVL1393/Asp2(a), pVL1393/Asp2(a)ΔTM and pVL1393/Asp2(a)ΔTM(His)₆. Creation of recombinant baculoviruses and infection of sf9 insect cells was performed using standard methods.

20 *Expression by transfection*

Transient and stable expression of Hu-Asp2(a)ΔTM and Hu-Asp2(a)ΔTM(His)₆ in High 5 insect cells was performed using the insect expression vector pIZ/V5-His. The DNA inserts from the expression plasmids vectors pVL1393/Asp2(a), pVL1393/Asp2(a)ΔTM and pVL1393/Asp2(a)ΔTM(His)₆ were 25 excised by double digestion with *Bam*H I and *Not*I and subcloned into *Bam*H I and *Not*I digested pIZ/V5-His using standard methods. The resulting expression plasmids, referred to as pIZ/Hu-Asp2ΔTM and pIZ/Hu-Asp2ΔTM(His)₆, were prepared as described above.

For transfection, High 5 insect cells were cultured in High Five serum free 30 medium supplemented with 10 µg/ml gentamycin at 27 °C in sealed flasks.

Transfections were performed using High five cells, High five serum free media supplemented with 10 µg/ml gentamycin, and InsectinPlus liposomes (Invitrogen, Carlsbad, CA) using standard methods.

For large scale transient transfections, 1.2 x 10⁷ high five cells were plated in a
5 150 mm tissue culture dish and allowed to attach at room temperature for 15-30 minutes. During the attachment time the DNA/ liposome mixture was prepared by mixing 6 ml of serum free media, 60 µg Hu-Asp2(a)ΔTM/pIZ (+/- His) DNA and 120 µl of Insectin Plus and incubating at room temperature for 15 minutes. The plating media was removed from the dish of cells and replaced with the DNA/liposome
10 mixture for 4 hours at room temperature with constant rocking at 2 rpm. An additional 6 ml of media was added to the dish prior to incubation for 4 days at 27 °C in a humid incubator. Four days post transfection the media was harvested, clarified by centrifugation at 500 x g, assayed for Hu-Asp2(a) expression by Western blotting. For stable expression, the cells were treated with 50 µg/ml Zeocin and the surviving
15 pool used to prepared clonal cells by limiting dilution followed by analysis of the expression level as noted above.

Purification of Hu-Asp2(a)ΔTM and Hu-Asp2(a)ΔTM(His)₆

Removal of the transmembrane segment from Hu-Asp2(a) resulted in the
20 secretion of the polypeptide into the culture medium. Following protein production by either baculovirus infection or transfection, the conditioned medium was harvested, clarified by centrifugation, and dialyzed against Tris-HCl (pH 8.0). This material was then purified by successive chromatography by anion exchange (Tris-HCl, pH 8.0) followed by cation exchange chromatography (Acetate buffer at pH 4.5) using NaCl
25 gradients. The elution profile was monitored by (1) Western blot analysis and (2) by activity assay using the peptide substrate described in Example 12. For the Hu-Asp2(a)ΔTM(His)₆, the conditioned medium was dialyzed against Tris buffer (pH 8.0) and purified by sequential chromatography on IMAC resin followed by anion exchange chromatography.

Amino-terminal sequence analysis of the purified Hu-Asp2(a)ΔTM(His)₆ protein revealed that the signal peptide had been cleaved [TQHGIRLPLR, corresponding to SEQ ID NO: 32, residues 22-3].

5

Example 11

Expression of Hu-Asp2(a) and Hu-Asp(b) in CHO cells

The materials (vectors, host cells, etc.) and methods described herein for expression of Hu-Asp2(a) are intended to be equally applicable for expression of Hu-Asp2(b).

10 *Heterologous expression of Hu-Asp-2(a) in CHO-K1 cells*

The entire coding sequence of Hu-Asp2(a) was cloned into the mammalian expression vector pcDNA3.1(+)Hygro (Invitrogen, Carlsbad, CA) which contains the CMV immediate early promoter and bGH polyadenylation signal to drive over expression. The expression plasmid, pcDNA3.1(+)Hygro/Hu-Asp2(a), was prepared by alkaline lysis and banding in CsCl and completely sequenced on both strands to verify the integrity of the coding sequence.

Wild-type Chinese hamster ovary cells (CHO-K1) were obtained from the ATCC. The cells were maintained in monolayer cultures in α-MEM containing 10% FCS at 37°C in 5% CO₂. Two 100 mm dishes of CHO-K1 cells (60% confluent) were transfected with pcDNA3.1(+)Hygro alone (mock) or pcDNA3.1(+)Hygro/Hu-Asp2(a) or pcDNA3.1(+)Hygro/Hu-Asp2(b) using the cationic liposome DOTAP as recommended by the supplier (Roche, Indianapolis, IN). The cells were treated with the plasmid DNA/liposome mixtures for 15 hours and then the medium replaced with growth medium containing 500 Units/ml hygromycin B. In the case of pcDNA3.1(+)Hygro/Hu-Asp2(a) or (b) transfected CHO-K1 cells, individual hygromycin B-resistant cells were cloned by limiting dilution. Following clonal expansion of the individual cell lines, expression of Hu-Asp2(a) or Hu-Asp2(b) protein was assessed by Western blot analysis using a polyclonal rabbit antiserum raised against recombinant Hu-Asp2 prepared by expression in *E. coli*. Near confluent dishes of each cell line were harvested by scraping into PBS and the cells

recovered by centrifugation. The cell pellets were resuspended in cold lysis buffer (25 mM Tris-HCl (pH 8.0)/5 mM EDTA) containing protease inhibitors and the cells lysed by sonication. The soluble and membrane fractions were separated by centrifugation (105,000 x g, 60 min) and normalized amounts of protein from each fraction were then separated by SDS-PAGE. Following electrotransfer of the separated polypeptides to PVDF membranes, Hu-Asp-2(a) or Hu-Asp2(b) protein was detected using rabbit anti-Hu-Asp2 antiserum (1/1000 dilution) and the antibody-antigen complexes were visualized using alkaline phosphatase conjugated goat anti-rabbit antibodies (1/2500). A specific immunoreactive protein with an apparent Mr value of 65 kDa was detected in pcDNA3.1(+)Hygro/Hu-Asp2 transfected cells and not mock-transfected cells. Also, the Hu-Asp2 polypeptide was only detected in the membrane fraction, consistent with the presence of a signal peptide and single transmembrane domain in the predicted sequence. Based on this analysis, clone #5 had the highest expression level of Hu-Asp2(a) protein and this production cell lines was scaled up to provide material for purification.

Purification of recombinant Hu-Asp-2(a) from CHO-K1/Hu-Asp2 clone #5

In a typical purification, clone #5 cell pellets derived from 20 150 mm dishes of confluent cells, were used as the starting material. The cell pellets were resuspended in 50 ml cold lysis buffer as described above. The cells were lysed by polytron homogenization (2 x 20 sec) and the lysate centrifuged at 338,000 x g for 20 minutes. The membrane pellet was then resuspended in 20 ml of cold lysis buffer containing 50 mM β -octylglucoside followed by rocking at 4 °C for 1 hour. The detergent extract was clarified by centrifugation at 338,000 x g for 20 minutes and the supernatant taken for further analysis.

The β -octylglucoside extract was applied to a Mono Q anion exchange column that was previously equilibrated with 25 mM Tris-HCl (pH 8.0)/50 mM β -octylglucoside. Following sample application, the column was eluted with a linear gradient of increasing NaCl concentration (0-1.0 M over 30 minutes) and individual fractions assayed by Western blot analysis and for β -secretase activity (see below). Fractions containing both Hu-Asp-2(a) immunoreactivity and β -secretase activity

were pooled and dialyzed against 25 mM NaOAc (pH 4.5)/50 mM β -octylglucoside. Following dialysis, precipitated material was removed by centrifugation and the soluble material chromatographed on a MonoS cation exchange column that was previously equilibrated in 25 mM NaOAc (pH 4.5)/ 50 mM β -octylglucoside. The 5 column was eluted using a linear gradient of increasing NaCl concentration (0-1.0 M over 30 minutes) and individual fractions assayed by Western blot analysis and for β -secretase activity. Fractions containing both Hu-Asp2 immunoreactivity and β -secretase activity were combined and determined to be >95% pure by SDS-PAGE/Coomassie Blue staining.

10 The same methods were used to express and purify Hu-Asp2(b).

Example 12

Assay of Hu-Asp2 β -secretase activity using peptide substrates

β -secretase assay

15 Recombinant human Asp2(a) prepared in CHO cells and purified as described in Example 11 was used to assay Asp2(a) proteolytic activity directly. Activity assays for Asp2(a) were performed using synthetic peptide substrates containing either the wild-type APP β -secretase site (SEVKM!DAEFR; SEQ ID NO: 64), the Swedish KM-NL mutation (SEVNL!DAEFR; SEQ ID NO: 63), or the A β 40 and 42 20 γ -secretase sites (RRGGVV!IA!TVIVGER; SEQ ID NO: 65). Reactions were performed in 50 mM 2-[N-morpholino]ethane-sulfonate ("Na-MES," pH 5.5) containing 1% β -octylglucoside, 70 mM peptide substrate, and recombinant Asp2(a) (1-5 μ g protein) for various times at 37°C. The reaction products were quantified by RP-HPLC using a linear gradient from 0-70 B over 30 minutes (A=0.1% TFA in water, B=0.1%TFA/10%water/90%AcCN). The elution profile was monitored by absorbance at 214 nm. In preliminary experiments, the two product peaks which 25 eluted before the intact peptide substrate, were confirmed to have the sequence DAEFR (SEQ ID NO: 72)and SEVNL (SEQ ID NO: 73) using both Edman sequencing and MADLI-TOF mass spectrometry. Percent hydrolysis of the peptide 30 substrate was calculated by comparing the integrated peak areas for the two product

peptides and the starting material derived from the absorbance at 214 nm. The sequence of cleavage/hydrolysis products was confirmed using Edman sequencing and MADLI-TOF mass spectrometry.

The behavior of purified Asp2(a) in the proteolysis assays was consistent with
5 the prior anti-sense studies which indicated that Asp2(a) possesses β -secretase activity. Maximal proteolysis was seen with the Swedish β -secretase peptide, which, after 6 hours, was about 10-fold higher than wild type APP.

The specificity of the protease cleavage reaction was determined by performing the β -secretase assay in the presence of 8 μ M pepstatin A and the presence
10 of a cocktail of protease inhibitors (10 μ M leupeptin, 10 μ M E64, and 5 mM EDTA). Proteolytic activity was insensitive to both the pepstatin and the cocktail, which are inhibitors of cathepsin D (and other aspartyl proteases), serine proteases, cysteinyl proteases, and metalloproteases, respectively.

Hu-Asp2(b) when similarly expressed in CHO cells and purified using
15 identical conditions for extraction with β -octylglucoside and sequential chromatography over Mono Q and Mono S also cleaves the Swedish β -secretase peptide in proteolysis assays using identical assay conditions.

Collectively, this data establishes that both forms of Asp2 (Hu-Asp2(a) and Hu-Asp2(b)) act directly in cell-free assays to cleave synthetic APP peptides at the β -secretase site, and that the rate of cleavage is greatly increased by the Swedish KM-NL mutation that is associated with Alzheimer's disease.
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An alternative β -secretase assay utilizes internally quenched fluorescent substrates to monitor enzyme activity using fluorescence spectroscopy in a single sample or multiwell format. Each reaction contained 50 mM Na-MES (pH 5.5),
25 peptide substrate MCA-EVKMDAEF[K-DNP] (SEQ ID NO: 71; BioSource International) (50 μ M) and purified Hu-Asp-2 enzyme. These components were equilibrated to 37 °C for various times and the reaction initiated by addition of substrate. Excitation was performed at 330 nm and the reaction kinetics were monitored by measuring the fluorescence emission at 390 nm. To detect compounds
30 that modulate Hu-Asp-2 activity, the test compounds were added during the

preincubation phase of the reaction and the kinetics of the reaction monitored as described above. Activators are scored as compounds that increase the rate of appearance of fluorescence while inhibitors decrease the rate of appearance of fluorescence.

5 It will be clear that the invention may be practiced otherwise than as particularly described in the foregoing description and examples.

Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, are within the scope of the invention. The entire disclosure of all publications cited herein are hereby incorporated by reference.

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What is claimed is:

1. A polypeptide comprising the amino acid sequence of a mammalian amyloid protein precursor (APP) or fragment thereof containing an APP cleavage site recognizable by a mammalian β -secretase, and further comprising two lysine residues at the carboxyl terminus of the amino acid sequence of the mammalian APP or APP fragment.
- 10 2. A polypeptide according to claim 1 comprising the amino acid sequence of a mammalian amyloid protein precursor (APP), and further comprising two lysine residues at the carboxyl terminus of the amino acid sequence of the mammalian amyloid protein precursor.
- 15 3. A polypeptide according to claim 1 wherein the polypeptide further includes a marker.
4. A polypeptide according to claim 3 wherein the marker comprises a reporter protein amino acid sequence attached to the APP amino acid sequence.
- 20 5. A polypeptide according to claim 4 wherein the reporter protein comprises an amino acid sequence of a fluorescing protein.
6. A polypeptide according to claim 1, wherein the mammalian APP is a human APP.
- 25 7. A polypeptide according to claim 6, wherein the human APP comprises at least one variation selected from the group consisting of a Swedish KM-NL mutation and a London V717-F mutation.

8. A polypeptide according to claim 6, wherein the human APP is selected from the group consisting of: an APP695 isoform, an APP 751 isoform, and an APP770 isoform.

5 9. A polypeptide according to claim 1 wherein the APP protein or fragment thereof comprises the APP-Sw β -secretase peptide sequence NLDA.

10 10. A polypeptide according to claim 9 wherein the APP protein or fragment thereof comprises the APP-Sw β -secretase peptide sequence
SEVNLDAEFR (SEQ ID NO: 63).

15 11. A polypeptide according to claim 9 wherein the APP protein or fragment thereof further includes an APP transmembrane domain carboxy-terminal to the APP-Sw β -secretase peptide sequence.

12. A polypeptide according to claim 9 wherein the APP protein or fragment thereof comprises a chimeric APP, said chimeric APP including partial APP amino acid sequences from at least two species.

20 13. A polypeptide according to claim 12 wherein the chimeric APP includes amino acid sequence of a human APP and a rodent APP.

14. A polynucleotide comprising a nucleotide sequence that encodes a polypeptide according to any one of claims 1.

25 15. A vector comprising a polynucleotide according to claim 14.

16. A vector according to claim 15 wherein said polynucleotide is operably linked to a promoter to promote expression of the polypeptide encoded by the
30 polynucleotide in a host cell.

17. A host cell transformed or transfected with a polynucleotide according to claim 14 or a vector according to claim 15 or 16.

18. A host cell according to claim 17 that is a mammalian cell.

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19. A polypeptide useful for assaying for modulators of β -secretase activity, said polypeptide comprising an amino acid sequence of the formula $\text{NH}_2\text{-X-Y-Z-KK-COOH}$;

wherein X, Y, and Z each comprise an amino acid sequence of at least 10 one amino acid;

wherein $\text{NH}_2\text{-X}$ comprises an amino-terminal amino acid sequence having at least one amino acid residue;

wherein Y comprises an amino acid sequence of a β -secretase recognition site of a mammalian amyloid protein precursor (APP); and

15 wherein Z-KK-COOH comprises a carboxy-terminal amino acid sequence ending in two lysine (K) residues.

20. A polypeptide according to claim 19 wherein the carboxyl-terminal amino acid sequence Z includes a hydrophobic domain that is a transmembrane domain in host cells that express the polypeptide.

21. A polypeptide according to claim 19 wherein the amino-terminal amino acid sequence X includes an amino acid sequence of a reporter protein.

25 22. A polypeptide according to claim 19 wherein the β -secretase recognition site Y comprises the human APP-Sw β -secretase peptide sequence NLDA.

30 23. A polynucleotide comprising a nucleotide sequence that encodes a polypeptide according to any one of claims 19-22.

24. A purified polypeptide comprising the murine Asp2 amino acid sequence set forth in SEQ ID NO: 8, or a fragment thereof that retains the β-secretase activity of said murine Asp2.

5 25. A polynucleotide comprising a nucleotide sequence that encodes the polypeptide of claim 24.

26. A polynucleotide according to claim 25 comprising the nucleotide sequence set forth in SEQ ID NO: 7.

10 27. A purified murine Asp2(b) polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 8 from residues 1-189 and 215-501, but lacking residues 190-214.

15 28. A polynucleotide comprising a nucleotide sequence that encodes the murine Asp2(b) polypeptide according to claim 27.

29. A vector comprising a polynucleotide according to claim 25.

20 30. A vector according to claim 29 wherein said polynucleotide is operably linked to a promoter to promote expression of the polypeptide encoded by the polynucleotide in a host cell.

25 31. A host cell transformed or transfected with a vector according to claim 30.

32. A host cell according to claim 31 that is a mammalian cell.

30 33. A host cell according to claim 31 that expresses the polypeptide on its surface.

34. A host cell according to claim 31, wherein the host cell is transfected with a nucleic acid comprising a nucleotide sequence that encodes an amyloid precursor protein (APP) that includes two carboxy-terminal lysine residues.

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35. A host cell according to claim 34 that expresses the polypeptide and the APP on its surface.

36. A method of making a murine Asp2 polypeptide comprising steps of
10 culturing a host cell of claim 61 in a culture medium under conditions in which the cell produces the polypeptide that is encoded by the polynucleotide.

37. A method according to claim 36, further comprising a step of purifying the polypeptide from the cell or the culture medium.

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38. A host cell transformed or transfected with a polynucleotide according to claim 25.

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39. A host cell according to claim 38 that is a mammalian cell.

40. A host cell according to claim 38 that expresses the polypeptide on its surface.

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41. A host cell according to claim 38, wherein the host cell is transfected with a nucleic acid comprising a nucleotide sequence that encodes an amyloid precursor protein (APP) or fragment thereof containing a β -secretase cleavage site.

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42. A host cell according to claim 41 wherein the APP includes two carboxy-terminal lysine residues.

43. A host cell according to claim 41 wherein the APP comprises the Swedish mutation (K→N, M→L) adjacent to the β-secretase cleavage site.

44. A host cell according to claim 41 that expresses the polypeptide and
5 the APP on its surface.

45. A method of making a murine Asp2 polypeptide comprising steps of culturing a host cell of claim 38 in a culture medium under conditions in which the cell produces the polypeptide that is encoded by the polynucleotide.

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46. A method according to claim 45, further comprising a step of purifying the polypeptide from the cell or the culture medium. –

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47. A purified polypeptide comprising a fragment of a mammalian Asp2 protein, wherein said polypeptide lacks the Asp2 transmembrane domain of said Asp2 protein, and wherein the polypeptide and the fragment retain the β-secretase activity of said mammalian Asp2 protein.

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48. A purified polypeptide according to claim 47 comprising a fragment of a human Asp2 protein that retains the β-secretase activity of said human Asp2 protein.

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49. A purified polypeptide according to claim 48, wherein said polypeptide comprises a fragment of Asp2(a) having the amino acid sequence set forth in SEQ ID NO: 4, and wherein said polypeptide lacks transmembrane domain amino acids 455 to 477 of SEQ ID NO: 4.

50. A purified polypeptide according to claim 49, wherein said polypeptide further lacks cytoplasmic domain amino acids 478 to 501 of SEQ ID NO: 4.

51. A purified polypeptide according to claim 50, wherein said polypeptide further lacks amino acids 420-454 of SEQ ID NO: 4.

52. A purified polypeptide according to any one of claims 48-51, wherein
5 said polypeptide comprises an amino acid sequence:

that includes amino acids 58 to 419 of SEQ ID NO: 4, and
that lacks amino acids 22 to 57 of SEQ ID NO: 4.

53. A purified polypeptide according to any one of claims 48-51, wherein
10 said polypeptide comprises an amino acid sequence:

that includes amino acids 46 to 419 of SEQ ID NO: 4, and
that lacks amino acids 22 to 45 of SEQ ID NO: 4.

54. A purified polypeptide according to claim 49, wherein said polypeptide
15 comprises an amino acid sequence that includes amino acids 22 to 454 of SEQ ID
NO: 4.

55. A purified polypeptide according to claim 47 comprising the amino
acid sequence of human Asp-2(b) protein set forth as SEQ ID NO: 6, or fragments
· 20 thereof that retain β-secretase activity.

56. A purified polypeptide according to claim 48, wherein said polypeptide
comprises a fragment of Asp2(b) having the amino acid sequence set forth in SEQ ID
NO: 6, and wherein said polypeptide lacks transmembrane domain amino acids 430 to
25 452 of SEQ ID NO: 6.

57. A purified polypeptide according to claim 56, wherein said polypeptide
further lacks cytoplasmic domain amino acids 453 to 476 of SEQ ID NO: 6.

58. A purified polypeptide according to claim 57, wherein said polypeptide further lacks amino acids 395-429 of SEQ ID NO: 4.

5 59. A purified polypeptide according to any one of claims 56-58, wherein said polypeptide comprises an amino acid sequence:

that includes amino acids 58 to 394 of SEQ ID NO: 4, and
that lacks amino acids 22 to 57 of SEQ ID NO: 4.

10 60. A purified polypeptide according to any one of claims 56-58, wherein said polypeptide comprises an amino acid sequence:

that includes amino acids 46 to 394 of SEQ ID NO: 4, and
that lacks amino acids 22 to 45 of SEQ ID NO: 4.

15 61. A purified polypeptide according to claim 56, wherein said polypeptide comprises an amino acid sequence that includes amino acids 22 to 429 of SEQ ID NO: 6.

20 62. A polypeptide comprising an amino acid sequence at least 95% identical to a fragment of a human Asp2 protein, wherein said polypeptide and said fragment lack a transmembrane domain and retain β-secretase activity of the human Asp2 protein.

25 63. A purified polynucleotide comprising a nucleotide sequence that encodes the polypeptide of any one of claims 47-63.

64. A polynucleotide of claim 47 wherein the polypeptide comprises a fragment of human Asp2 protein.

30 65. A polynucleotide of claim 64 wherein the polypeptide comprises a fragment of Asp2(a) having the amino acid sequence set forth as SEQ ID NO: 4, and

wherein the polypeptide lacks the transmembrane domain amino acids 455-477 of SEQ ID NO: 4.

5 66. A polynucleotide of claim 64, wherein the polypeptide further lacks cytoplasmic domain amino acids 478-501 of SEQ ID NO: 4.

67. A purified polynucleotide of claim 66, wherein said polypeptide further lacks amino acids 420-454 of SEQ ID NO: 4.

10 68. A polynucleotide of claim 65, wherein the polypeptide comprises an amino acid sequence:

that includes amino acids 58-419 of SEQ ID NO: 4, and
that lacks amino acids 22-57 of SEQ ID NO: 4.

15 69. A polynucleotide of claim 65, wherein the polypeptide comprises an amino acid sequence:

that includes amino acids 46-419 of SEQ ID NO: 4, and
that lacks amino acids 22-45 of SEQ ID NO: 4.

20 70. A polynucleotide of claim 65, wherein the polypeptide comprises an amino acid sequence that includes amino acids 22-454 of SEQ ID NO: 4.

25 71. A polynucleotide of claim 64, wherein the polypeptide comprises a fragment of human Asp2(b) having the amino acid set forth in SEQ ID NO: 6, and
wherein the polypeptide lacks transmembrane domain amino acids 430-452 of SEQ ID NO: 6.

72. A polynucleotide of claim 71, wherein the polypeptide lacks cytoplasmic domain amino acids 453-476 of SEQ ID NO: 6.

73. A polynucleotide of claim 72, wherein the polypeptide further lacks amino acids 395-429 of SEQ ID NO: 6.

74. A polynucleotide of claim 71, wherein the polypeptide comprises an 5 amino acid sequence:

that includes amino acids 58-394 of SEQ ID NO: 6, and
that lacks amino acids 22 to 57 of SEQ ID NO: 6.

75. A polynucleotide of claim 71, wherein the polypeptide comprises an 10 amino acid sequence:

that includes amino acids 46-394 of SEQ ID NO: 6, and
that lacks amino acids 22-45 of SEQ ID NO: 6.

76. A polynucleotide of claim 71, wherein the polypeptide comprises an 15 amino acid sequence that includes amino acids 22 to 429 of SEQ ID NO: 6.

77. A vector comprising a polynucleotide according to claim 63.

20 78. A host cell transformed or transfected with a polynucleotide according to claim 63.

79. A host cell transformed or transfected with a vector of claim 77.

25 80. A polynucleotide comprising a nucleotide sequence that hybridizes under stringent conditions to a nucleic acid comprising the sequence set forth in SEQ ID NO: 4 or SEQ ID NO: 6, wherein the nucleotide sequence encodes a polypeptide having β-secretase biological activity.

30 81. A vector comprising a polynucleotide of claim 80.

82. A host cell transformed or transfected with a polynucleotide of claim
80.

83. A method for assaying for modulators of β -secretase activity,
5 comprising the steps of:

- (a) contacting a first composition with a second composition both in the presence and in the absence of a putative modulator compound, wherein the first composition comprises a mammalian β -secretase polypeptide or biologically active fragment thereof, and wherein the second composition comprises a substrate 10 polypeptide having an amino acid sequence comprising a β -secretase cleavage site;
- (b) measuring cleavage of the substrate polypeptide in the presence and in the absence of the putative modulator compound; and
- (c) identifying modulators of β -secretase activity from a difference in cleavage in the presence versus in the absence of the putative modulator compound, 15 wherein a modulator that is a β -secretase antagonist reduces such cleavage and a modulator that is a β -secretase agonist increases such cleavage.

84. A method according to claim 83, wherein the first composition
comprises a purified human Asp2 polypeptide.

20 85. A method according to claim 83, wherein the first composition
comprises a soluble fragment of a human Asp2 polypeptide that retains Asp2 β -secretase activity.

25 86. A method according to claim 85 wherein the soluble fragment is a
fragment lacking an Asp2 transmembrane domain.

87. A method according to claim 83, wherein the substrate polypeptide of
the second composition comprises the amino acid sequence SEVNLDAEFR.

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88. A method according to claim 83, wherein the substrate polypeptide of the second composition comprises the amino acid sequence EVKMDAEF.

89. A method according to claim 83, wherein the second composition
5 comprises a polypeptide having an amino acid sequence of a human amyloid precursor protein (APP).

90. A method according to claim 89, wherein the human amyloid precursor protein is selected from the group consisting of: APP695, APP751, and APP770.

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91. A method according to claim 90, wherein the human amyloid precursor protein includes at least one mutation selected from a KM-NL Swiss mutation and a V-F London mutation.

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92. A method according to claim 89, wherein the polypeptide having an amino acid sequence of a human APP further comprises an amino acid sequence comprising a marker sequence attached amino-terminal to the amino acid sequence of the human amyloid precursor protein.

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93. A method according to claim 89, wherein the polypeptide having an amino acid sequence of a human APP further comprises two lysine residues attached to the carboxyl terminus of the amino acid sequence of the human APP.

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94. A method according to claim 82, wherein the second composition comprises a eukaryotic cell that expresses amyloid precursor protein (APP) or a fragment thereof containing a β -secretase cleavage site.

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95. A method according to claim 94, wherein the APP expressed by the host cell is an APP variant that includes two carboxyl-terminal lysine residues.

96. A method for identifying agents that inhibit the activity of human Asp2 aspartyl protease (Hu-Asp2), comprising the steps of:

(a) contacting amyloid precursor protein (APP) and purified and isolated

Hu-Asp2 in the presence and absence of a test agent;

5 (b) determining the APP processing activity of the Hu-Asp2 in the presence and absence of the test agent; and

10 (c) comparing the APP processing activity of the Hu-Asp2 polypeptide in the presence of the test agent to the activity in the absence of the test agent to identify an agent that inhibits the APP processing activity of Hu-Asp2, wherein reduced activity in the presence of the test agent identifies an agent that inhibits Hu-Asp2 activity.

15 97. A method according to claim 96, wherein the Hu-Asp2 comprises a polypeptide purified and isolated from a cell transformed or transfected with a polynucleotide comprising a nucleotide sequence that encodes the Hu-Asp2.

98. A method according to claim 60 wherein the nucleotide sequence is selected from the group consisting of:

20 (a) a nucleotide sequence encoding the Hu-Asp2(a) amino acid sequence set forth in SEQ ID NO: 4;

(b) a nucleotide sequence encoding the Hu-Asp2(b) amino acid sequence set forth in SEQ ID NO: 6;

25 (c) a nucleotide sequence encoding a fragment of Hu-Asp2(a) (SEQ ID NO: 4) or Hu-Asp2(b) (SEQ ID NO: 6), wherein said fragment exhibits aspartyl protease activity characteristic of Hu-Asp2(a) or Hu-Asp2(b); and

(d) a nucleotide sequence of a polynucleotide that hybridizes under stringent hybridization conditions to the complement of a Hu-Asp2-encoding polynucleotide selected from the group consisting of SEQ ID NO: 3 and SEQ ID NO: 30 5.

99. A method according to claim 97 wherein the Hu-Asp2 comprises the Hu-Asp2(a) amino acid sequence set forth in SEQ ID NO: 4.

5 100. A method according to claim 97, wherein the Hu-Asp2 comprises the Hu-Asp2(b) amino acid sequence set forth in SEQ ID NO: 6.

10 101. A method according to claim 97, wherein the Hu-Asp2 comprises a fragment of Hu-Asp2(a) (SEQ ID NO: 4) or Hu-Asp2(b) (SEQ ID NO: 6), wherein said fragment exhibits aspartyl protease activity characteristic of Hu-Asp2(a) or Hu-Asp2(b).

15 102. A method according to claim 96, wherein the APP comprises the Swedish mutation (K→N, M→L) adjacent to the β-secretase processing site.

103. A method according to claim 96, further comprising a step of treating Alzheimer's Disease with an agent identified as an inhibitor of Hu-Asp2 according to steps (a)-(c).

20 104. A method for identifying agents that inhibit the activity of human Asp2 aspartyl protease (Hu-Asp2), comprising the steps of:

- (a) contacting Hu-Asp2 and amyloid precursor protein (APP) in the presence and absence of a test agent, wherein the APP comprises a carboxy-terminal di-lysine (KK) and wherein the contacting comprises growing a host cell that expresses the APP in the presence and absence of the test agent;
- (b) determining the APP processing activity of the Hu-Asp2 in the presence and absence of the test agent; and
- (c) comparing the APP processing activity of the Hu-Asp2 polypeptide in the presence of the test agent to the activity in the absence of the test agent to identify an agent that inhibits the activity of Hu-Asp2, wherein reduced

activity in the presence of the test agent identifies an agent that inhibits Hu-Asp2 activity.

105. A method according to claim 104, wherein the APP further comprises
5 the Swedish mutation (K→N, M→L) adjacent to the β-secretase processing site.

106. A method according to claim 104, wherein the host cell has been
transformed or transfected with a polynucleotide comprising a nucleotide sequence
that encodes a Hu-Asp2, wherein said nucleotide sequence is selected from the group
10 consisting of:

- (a) a nucleotide sequence encoding the Hu-Asp2(a) amino acid sequence set forth in SEQ ID NO: 4;
- (b) a nucleotide sequence encoding the Hu-Asp2(b) amino acid sequence set forth in SEQ ID NO: 6;
- 15 (c) a nucleotide sequence encoding a fragment of Hu-Asp2(a) (SEQ ID NO: 4) or Hu-Asp2(b) (SEQ ID NO: 6), wherein said fragment exhibits aspartyl protease activity characteristic of Hu-Asp2(a) or Hu-Asp2(b); and
- (d) a nucleotide sequence of a polynucleotide that hybridizes under stringent hybridization conditions to the complement of a Hu-Asp2-encoding
20 polynucleotide selected from the group consisting of SEQ ID NO: 3 and SEQ ID NO: 5.

107. A method according to claim 104, further comprising a step of treating Alzheimer's Disease with an agent identified as an inhibitor of Hu-Asp2 according to
25 steps (a)-(c).

108. A method for identifying agents that inhibit the activity of human Asp2 aspartyl protease (Hu-Asp2), comprising the steps of:
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- (a) contacting Hu-Asp2 and amyloid precursor protein (APP) in the presence and absence of a test agent, wherein the contacting comprises

growing a host cell transformed or transfected with a polynucleotide comprising a nucleotide sequence encoding the Hu-Asp2 in the presence and absence of the test agent;

5 (b) determining the APP processing activity of the Hu-Asp2 in the presence and absence of the test agent; and

(c) comparing the APP processing activity of the Hu-Asp2 polypeptide in the presence of the test agent to the activity in the absence of the test agent to identify an agent that inhibits the activity of Hu-Asp2, wherein reduced activity in the presence of the test agent identifies an agent that inhibits Hu-

10 Asp2 activity.

109. A method according to claim 108, wherein the host cell expresses APP:

110. A method according to claim 109 wherein the determining step
15 comprises measuring the production of amyloid beta peptide by the cell in the presence and absence of the test agent.

111. A method according to claim 109, wherein the host cell expresses an APP having an amino acid sequence that includes a carboxy-terminal di-lysine.

20 112. A method according to claim 109, wherein the host cell expresses an APP comprising the Swedish mutation (K→N, M→L) adjacent to the β-secretase processing site.

25 113. A method according to claim 108, wherein the host cell is a human embryonic kidney cell line 293 (HEK293) cell.

114. A method according to claim 108 wherein the nucleotide sequence is selected from the group consisting of:

(a) a nucleotide sequence encoding the Hu-Asp2(a) amino acid sequence set forth in SEQ ID NO: 4;

5 (b) a nucleotide sequence encoding the Hu-Asp2(b) amino acid sequence set forth in SEQ ID NO: 6;

(c) a nucleotide sequence encoding a fragment of Hu-Asp2(a) (SEQ ID NO: 4) or Hu-Asp2(b) (SEQ ID NO: 6), wherein said fragment exhibits aspartyl protease activity characteristic of Hu-Asp2(a) or Hu-Asp2(b); and

10 (d) a nucleotide sequence of a polynucleotide that hybridizes under stringent hybridization conditions to the complement of a Hu-Asp2-encoding polynucleotide selected from the group consisting of SEQ ID NO: 3 and SEQ ID NO: 5.

15 115. A method according to claim 108, wherein the host cell comprises a vector that comprises the polynucleotide.

20 116. A method according to claim 108 wherein the polynucleotide comprises a nucleotide sequence encoding the Hu-Asp2(a) amino acid sequence set forth in SEQ ID NO: 4.

117. A method according to claim 108 wherein the polynucleotide comprises a nucleotide sequence encoding the Hu-Asp2(b) amino acid sequence set forth in SEQ ID NO: 6.

25 118. A method according to claim 108 wherein the polynucleotide comprises a nucleotide sequence encoding a polypeptide comprising a fragment of Hu-Asp2(a) (SEQ ID NO: 4) or Hu-Asp2(b) (SEQ ID NO: 6), wherein said fragment exhibits aspartyl protease activity characteristic of Hu-Asp2(a) or Hu-Asp2(b).

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119. A method according to claim 108 wherein the Hu-Asp2 is encoded by a nucleotide sequence of a polynucleotide that hybridizes under stringent hybridization conditions to the complement of a Hu-Asp2-encoding polynucleotide selected from the group consisting of SEQ ID NO: 3 and SEQ ID NO: 5.

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120. A method according to claim 108, further comprising a step of treating Alzheimer's Disease with an agent identified as an inhibitor of Hu-Asp2 according to steps (a)-(c).

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121. A method for identifying agents that modulate the activity of Asp2 aspartyl protease, comprising the steps of:

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(a) contacting an Asp2 aspartyl protease and amyloid precursor protein (APP) in the presence and absence of a test agent, wherein the Asp2 aspartyl protease is encoded by a nucleic acid molecule that hybridizes under stringent hybridization conditions to the complement of a Hu-Asp2-encoding polynucleotide selected from the group consisting of SEQ ID NO: 3 and SEQ ID NO: 5;

(b) determining the APP processing activity of the Asp2 aspartyl protease in the presence and absence of the test agent; and

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(c) comparing the APP processing activity of the Asp2 aspartyl protease in the presence of the test agent to the activity in the absence of the agent to identify agents that modulate the activity of the Asp2 aspartyl protease, wherein a modulator that is an Asp2 inhibitor reduces APP processing and a modulator that is an Asp2 agonist increases such processing.

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122. A method according to claim 121, wherein the Asp2 aspartyl protease is purified and isolated.

30

123. A method according to claim 121, further comprising a step of treating Alzheimer's Disease with an agent identified as an inhibitor of Hu-Asp2 according to steps (a)-(c).

124. A method for identifying an agent that inhibits APP processing activity of human Asp2 aspartyl protease, comprising steps of:

- (a) contacting Hu-Asp2 with an APP substrate for the Hu-Asp2, in the presence and absence of a test agent;
- 5 (b) determining the proteolytic processing of the APP substrate by the Hu-Asp2 in the presence and absence of the test agent; and
- (c) comparing the proteolytic processing of the APP substrate by the Hu-Asp2 in the presence and absence of the test agent to identify an agent that inhibits the APP processing activity of Hu-Asp2, wherein reduced proteolytic processing of the
- 10 APP substrate by the Hu-Asp2 in the presence of the test agent identifies an agent that inhibits Hu-Asp2 activity.

125. A method according to claim 124, wherein the APP substrate is a peptide comprising a β-secretase cleavage site of APP.

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126. A method according to claim 125, wherein the β-secretase cleavage site comprises the formula P2-P1-P1'-P2', wherein

P2 is an amino acid selected from K and N;

P1 is an amino acid selected from M and L;

20 P1' is the amino acid D; and

P2' is the amino acid A.

127. A method according to claim 125, wherein the peptide comprises the amino acid sequence KMDA (SEQ ID NO: 64, positions 4-7).

25

128. A method according to claim 126, wherein the peptide comprises the amino acid sequence EVKMDAEF (SEQ ID NO: 67).

30 129. A method according to claim 125, wherein the peptide comprises the amino acid sequence NLDA (SEQ ID NO: 66).

130. A method of reducing cellular production of amyloid beta (A β) from amyloid precursor protein (APP), comprising step of transforming or transfecting cells with an anti-sense reagent capable of reducing Asp2 polypeptide production by
5 reducing Asp2 transcription or translation in the cells, wherein reduced Asp2 polypeptide production in the cells correlates with reduced cellular processing of APP into A β .

131. A method according to claim 130, wherein the cell is a neural cell.
10

132. A method according to claim 130, wherein the anti-sense reagent comprises an oligonucleotide comprising a single stranded nucleic acid sequence capable of binding to a Hu-Asp mRNA.

15 133. A method according to claim 130, wherein the anti-sense reagent comprises an oligonucleotide comprising a single stranded nucleic acid sequence capable of binding to a Hu-Asp DNA.

20 134. A method of reducing cellular production of amyloid beta (A β) from amyloid precursor protein (APP), comprising steps of:
(a) identifying mammalian cells that produce A β ; and
(b) transforming or transfecting the cells with an anti-sense reagent capable of reducing Asp2 polypeptide production by reducing Asp2 transcription or translation in the cells, wherein reduced Asp2 polypeptide production in the cells correlates with reduced cellular processing of APP into
25 A β .

135. A method according to claim 134, wherein the cell is a neural cell.

136. A method according to claim 134, wherein the anti-sense reagent comprises an oligonucleotide comprising a single stranded nucleic acid sequence capable of binding to a Hu-Asp mRNA.

5 137. A method according to claim 133, wherein the anti-sense reagent comprises an oligonucleotide comprising a single stranded nucleic acid sequence capable of binding to a Hu-Asp DNA.

10 138. A method according to claim 133, wherein the identifying step comprises diagnosing Alzheimer's disease, where Alzheimer's disease correlates with the existence of cells that produce A β that forms amyloid plaques in the brain.

15 139. A vector comprising a polynucleotide according to claim 22.

140. A host cell comprising a vector according to claim 139.

141. A purified polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 8.

20 142. A polypeptide comprising an amino acid sequence at least 95% identical to a polypeptide according to any one of claims 42-61, wherein said polypeptide lacks a transmembrane domain and retains β -secretase activity of a human Asp2 protein.

25 143. A method according to claim 83, wherein the first composition comprises a human Asp2 polypeptide of any one of claims 1-13, 19-24, 26-27 or 47-62.

144. A method according to claim 124 wherein the Hu-Asp2 is purified and isolated.

145. A method according to claim 124, wherein the Hu-Asp2 is encoded by
5 a nucleic acid that hybridizes under stringent hybridization conditions to the complement of a Hu-Asp2-encoding polynucleotide selected from the group consisting of SEQ ID NO: 3 and SEQ ID NO: 5.

146. A method according to claim 124, wherein the Hu-Asp2 is selected
10 from the group consisting of:

- (a) Hu-Asp2(a) comprising the amino acid sequence set forth in SEQ ID NO: 4;
- (b) Hu-Asp2(b) comprising the amino acid sequence set forth in SEQ ID NO: 6; and
- 15 (c) fragments of Hu-Asp2(a) (SEQ ID NO: 4) and Hu-Asp2(b) (SEQ ID NO: 6) that cleave the APP substrate at a β -secretase cleavage site.

147. A method according to claim 87, wherein the Hu-Asp2 comprises an amino acid sequence at least 95% identical to an amino acid sequence selected from
20 the group consisting of SEQ ID NOS: 4 and 6.

148. A method according to claim 146, wherein the Hu-Asp2 comprises a soluble fragment of Hu-Asp2(a) or Hu-Asp2(b) that lacks an Asp2 transmembrane domain.

25

149. A method according to claim 148, wherein the Hu-Asp2 has an amino acid sequence consisting of a sequence-selected from the group consisting of SEQ ID NOS: 30, 32, 51, and 53.

150. A method according to claim 148, wherein the Hu-Asp2 comprises a fragment of Hu-Asp2(a) or Hu-Asp2(b), wherein the Hu-Asp 2 lacks amino acids 1-45 of SEQ ID NOS: 4 or 6.

FIGURE 1A

ATGGGCGCACTGGCCCG GCGCTGCTGCTG CCTCTGCTGGCC CAGTGGCTCCTG CGGCC
 M G A L A R A L L P L L A Q W L L R A
 CCCCGGAGCTGGCCCCCG CGCCCTCACGC TGCCCCCTCCGGG TGGCCGCGGCCA CGAAC
 A P E L A P A P F T L P L R V A A A T N
 CGCGTAGTTGCGCCACC CGGGGACCCGG ACCCGTCCGAG CGCCACGCCGAC GGCTTG
 R V V A P T P G P G T P A E R H A D G L
 GCGCTCGCCCTGGAGCCT GCCCTGGGTCC CCCGCGGCCGCCA GCAAATTCTTG GCCATG
 A L A L E P A L A S P A G A A N F L A M
 GTAGACAACCTGCAGGGG GACTCTGCCGC GGCTACTACCTGGAGATGCTGATC GGGACC
 V D N L Q G D S G R G Y Y L E M L I G T

 CCCCCG CAGAAGCTACAG ATTCTCGTTGAC ACTGGAAGCAGT AACCTTGCCGTG GCAGGA
 P P Q K L Q I L V D T G S S N F A V A G

 ACCCCG CACTCCTACATA GACACGTACTTT GACACAGAGAGG TCTAGCACATAC CGCTCC
 T P H S Y I D T Y F D T E R S S T Y R S

 AAGGGCTTGACGTACACA GTGAAGTACACA CAAGGAAGCTGG ACGGGCTTCGTT GGGGAA
 K G F D V T V K Y T Q G S W T G F V G E

 GACCTCGTACCATCCCC AAAGGCTTCAT ACTTCTTTCTT GTCAACATTGCC ACTATT
 D L V T I P K G F N T S F L V N I A T I

 TTTGAATCAGAGAATTTC TTTTGCCCTGGG ATTAATGGAAT GGAATACCTGGC CTAGCT
 F E S E N F F L P G I K W N G I L G L A

 TATGCCACACTGCCAAG CCATCAAGTTCT CTGGAGACCTTC TTCGACTCCCTG GTGACA
 Y A T L A K P S S S L E T F F D S L V T

 CAAGCAAACATCCCCAAC GTTTCTCCATG CAGATGTGTGGA GCCGGCTTGCCC GTTGCT
 Q A N I P N V F S M Q M C G A G L P V A

 GGATCTGGACCAACGGA GGTAGTCTTGTCTTGGGTGGAATT GAACCAAGTTG TATAAA
 G S G T N G G S L V L G G I E P S L Y K

 GGAGACATCTGGTATACC CCTATTAAAGGAA GAGTGGTACTAC CAGATAGAAATT CTGAAA
 G D I W Y T P I K E E W Y Y Q I E I L K

 TTGGAAATTGGAGGCCAA AGCTTAATCTG GACTGCAGAGAG TATAACGCAGAC AAGGCC
 L E I G G Q S L N L D C R E Y N A D K A

 ATCGTGGACAGTGGCACC ACGCTGCTGCGC CTGGCCAGAAG GTGTTGATGCG GTGGTG
 I V D S G T T L L R L P Q K V F D A V V

 GAAGCTGTGGCCCGCGCA TCTCTGATTCCA GAATTCTCTGAT GTGTTCTGGACT GGGTCC
 E A V A R A S L I P E F S D G F W T G S

 CAGCTGGCGTGGACGAAATCGGAAACA CCTTGGTCTTAC TTCCCTAAATCTCCATC
 Q L A C W T N S E T P W S Y F P K I S I

 TACCTGAGAGATGAGAAC TCCAGCAGGTCA TTCCGTATCACA ATCCTGCCCTAG CTTTAC
 Y L R D E N S S R S F R I T I L P Q L Y

 ATTCAAGCCATGATGGGG GCCGGCCTGAAT TATGAATGTTAC CGATTGGCATT TCCCCA
 I Q P M M G A G L N Y E C Y R F G I S P

 TCCACAAATGGCTGGTATCGGTGCCACG GTGATGGAGGGC TTCTACGTCACT TTGAC
 S T N A L V I G A T V M E G F Y V I F D

 AGAGCC CAGAAGAGGGTG GGCTTCGAGCG AGCCCTGTGCA GAAATTGCAGGT GCTGCA

FIGURE 1B

R A Q K R V G F A A S P C A E I A G A A
GTGTCTGAAATTCCGGGCCTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT
V S E I S G P F S T E D V A S N C V P A
CAGTCCTTGAGCGAGCCCATTGTGGATTGTGTCTATGCCCTCATGAGCGTCTGTGGA
Q S L S E P I L W I V S Y A L M S V C G
GCCATCCTCCTGTCTTAATCGTCCTGCTGCTGCCGTTCCGGTGTCAAGCGTCGCC
A I L L V L I V L L L P F R C Q R R P
CGTGACCCCTGAGGTCGTCAATGATGAGTCCTCTGGTCAGACATCGCTGGAAATGAATA
R D P E V V N D E S S L V R H R W K
GCCAGGCCTGACCTCAAGCAACCATGAACACTAGCTATTAAGAAAATCACATTCCAGGGC
AGCAGCCGGGATCGATGGTGGCGTTCTCCTGTGCCAACCGTCTCAATCTCTGTTCT
GCTCCCAGATGCCTCTAGATTCAGTCACTGTCTTGATTCTCAAGCTTCAAATC
CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAACTTCATTCTAAACCAAAAAAAA
AAAA

FIGURE 2A

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGCGCGGGAGTGCTGCCTGCCAC
 M A Q A L P W L L W M G A G V L P A H

 GGCACCCAGCACGGCATC CGGCTGCCCTG CGCAGCGGCTGGGGGCCCGGGCTGG
 G T Q H G I R L P L R S G L G G A P L G

 CTGCGGCTGCCCGGGAG ACCGACGAAGAG CCCGAGGAGCCC GGCGGGAGGGC AGCTTT
 L R L P R E T D E E P E E P G R R G S F

 GTGGAGATGGTGGACAAC CTGAGGGCAAG TCGGGGAGGGC TACTACGTGGAG ATGACC
 V E M V D N L R G K S G Q G Y Y V E M T

 GTGGGCA GCCCCCCCGAG ACGCTAACATC CTGGTGGATACA GGCAAGCAGTAAC TTTGCA
 V G S P P Q T L N I L V D T G S S N F A

 GTGGGTGCTGCCCTGCAT CCCTTCCTGCAT CGCTACTACCAG AGGCAGCTGTCC AGCACA
 V G A A P H P F L H R Y Y Q R Q L S S T

 TACCGGGACCTCCGGAAG GGTGTGTATGTG CCCTACACCCAG GGCAAGTGGAA GGGGAG
 Y R D L R K G V Y V P Y T Q G K W E G E

 CTGGGCA CCGACCTGGTA AGCATCCCCAT GGCCCCAACGTC ACTGTGCGTGCC AACATT
 L G T D L V S I P H G P N V T V R A N I

 GCTGCCATCACTGAATCA GACAAGTTCTTC ATCAACGGCTCC AACTGGGAAGGC ATCCTG
 A A I T E S D K F F I N G S N W E G I L

 GGGCTGGCTATGCTGAG ATTGCCAGGCTT TGTGGTGTGGC TTCCCCCTCAAC CAGTCT
 G L A Y A E I A R L C G A G F P L N Q S

 GAAGTGTGGCTCTGTC GGAGGGAGCATG ATCATTGGAGGT ATCGACCACTCG CTGTAC
 E V L A S V G G S M I I G G I D H S L Y

 ACAGGCAGTCTCTGGTAT ACACCCATCCGG CGGGAGTGGTAT TATGAGGTGATC ATTGTG
 T G S L W Y T P I R R E W Y Y E V I I V

 CGGGTGGAGATCAATGGA CAGGATCTGAAA ATGGACTGCAAG GAGTACAACATGACAAG
 R V E I N G Q D L K M D C K E Y N Y D K

 AGCATTGTGGACAGTGGC ACCACCAACCTT CGTTTGCCTAAG AAAGTGTGAA GCTGCA
 S I V D S G T T N L R L P K K V F E A A

 GTCAAATCCATCAAGGCA GCCTCCCTCCACG GAGAAGTCCCT GATGGTTCTGG CTAGGA
 V K S I K A A S S T E K F P D G F W L G

 GAGCAGCTGGTGTGCTGG CAAGCAGGCACC ACCCCTTGGAAC ATTTTCCAGTC ATCTCA
 E Q L V C W Q A G T T P W N I F P V I S

 CTCTACCTAATGGGTGAG GTTACCAACAG TCCTTCCGCATC ACCATCCTCCG CAGCAA
 L Y L M G E V T N Q S F R I T I L P Q Q

 TACCTGCGGCCAGTGGAA GATGTGGCCACG TCCCAAGACGAC TGTTACAAGTTGCCATC

FIGURE 2B

Y L R P V E D V A T S Q D D C Y K F A I
 TCACAGTCATCCACGGGC ACTGTTATGGGA GCTGTTATCATG GAGGGCTTCTAC GTTGTC
 S Q S S T G T V M G A V I M E G F Y V V
 TTTGATCGGGCCGAAAA CGAATTGGCTTT GCTGTCAGCGCT TGCCATGTGCAC GATGAG
 F D R A R K R I G F A V S A C H V H D E
 TTCAGGACGGCAGCGGTG GAAGGCCCTTT GTCACCTTGGAC ATGGAAGACTGT GGCTAC
 F R T A A V E G P F V T L D M E D C G Y
 AACATTCCACAGACAGAT GAGTCACCCCTC ATGACCATAGCC TATGTCATGGCT GCCATC
 N I P Q T D E S T L M T I A Y V M A A I
 TGCGCCCTCTTCATGCTG CCACTCTGCCTC ATGGTGTGTCAG TGGCGCTGCCTC CGCTGC
 C A L F M L P L C L M V C Q W R C L R C
 CTGCGCCAGCAGCATGAT GACTTTGCTGAT GACATCTCCCTG CTGAAGTGAGGA GGCCCA
 L R Q Q H D D F A D D I S L L K
 TGGGCA GAAGATAGAGAT TCCCCTGGACCA CACCTCCGTGGT TCACTTTGGTCA CAAGTA
 GGAGAC ACAGATGGCACC TGTGGCCAGAGC ACCTCAGGACCC TCCCCACCCACC AAATGC
 CTCTGC CTTGATGGAGAA GGAAAAGGCTGG CAAGGTGGGTTTC CAGGGACTGTAC CTGTAG
 GAAACA GAAAAGAGAAGA AAGAACACTCT GCTGGCGGAAT ACTCTTGGTCAC CTCAA
 TTAAAG TCGGGAAATTCT GCTGCTGAAAC TTCAGCCCTGAA CCTTTGTCACC ATTCT
 TTAAAT TCTCCAACCCAA AGTATTCTCTT TTCTTAGTTCA GAAGTACTGGCA TCACAC
 GCAGGT TACCTTGCGTG TGTCCCTGTGGT ACCCTGGCAGAG AAGAGACCAAGC TTGTT
 CCCTGCTGGCCAAAGTCA GTAGGAGAGGAT GCACAGTTGCT ATTTGCTT TAGA GACAGG
 GACTGTATAAACAGCCT AACATTGGTCA AAGATTGCCT TGAAAAAAAAAAA AAA

FIGURE 3A

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGCGCGGGAGTGCTGCCTGCCAC
 M A Q A L P W L L L W M G A G V L P A H

 GGCACCCAGCACGGCATCGGCTGCCCTGCGCAGCGGCCCTGGGGCGCCCCCTGGGG
 G T Q H G I R L P L R S G L G G A P L G

 CTGCGGCTGCCCGGGAGACCGACGAAGAGCCGAGGAGCCC GGCGGGAGGGCAGCTTT
 L R L P R E T D E E P E E P G R R G S F

 GTGGAGATGGTGGACAACCTGAGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC
 V E M V D N L R G K S G Q G Y Y V E M T

 GTGGGCAGCCCCCGCAGACGCTAACATCCTGGTGGATACAGGCAGCAGTAACTTGCA
 V G S P P Q T L N I L V D T G S S N F A

 GTGGGTGCTGCCACACCCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA
 V G A A P H P F L H R Y Y Q R Q L S S T

 TACCGGGACCTCCGGAAGGGTGTATGTGCCCTACACCCAGGGCAAGTGGAAGGAG
 Y R D L R K G V Y V P Y T Q G K W E G E

 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT
 L G T D L V S I P H G P N V T V R A N I

 GCTGCCATCACTGAATCA GACAAGTTCTTCATCAACGGCTCAAATGGGAAGGCATCTG
 A A I T E S D K F F I N G S N W E G I L

 GGGCTGGCTATGCTGAGATTGCCAGGCCTGACCACTCCCTGGAGCTCTTCTTTGACTCT
 G L A Y A E I A R P D D S L E P F F D S

 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTGGCAGCTTGTTGCTGGCTTC
 L V K Q T H V P N L F S L Q L C G A G F

 CCCCTCAACCAGTCTGAAAGTGGCTGGCTCTGTGGAGGGAGCATGATCATTGGAGGTATC
 P L N Q S E V L A S V G G S M I I G G I

 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATC CGGCGGGAGTGGTATTAT
 D H S L Y T G S L W Y T P I R R E W Y Y

 GAGGTCACTATTGTGCGG GTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG
 E V I I V R V E I N G Q D L K M D C K E

 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCCACCTTCGTTGCCCAAGAAA
 Y N Y D K S I V D S G T T N L R L P K K

 GTGTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCACGGAGAAGTTCCTGAT
 V F E A A V K S I K A A S S T E K F P D

FIGURE 3B

GGTTTCTGGCTAGGAGAG CAGCTGGTGTGC TGGCAAGCAGGC ACCACCCCTGG AACATT
 G F W L G E Q L V C W Q A G T T P W N I

 TTCCCAGTCATCTCACTCTACCTAATGGGT GAGGTTACCAAC CAGTCCTTCCGC ATCAC
 F P V I S L Y L M G E V T N Q S F R I T

 ATCCCTCCGCAAGCAATAC CTGCGGCCAGTG GAAGATGTGGCC ACGTCCAAGAC GACTGT
 I L P Q Q Y L R P V E D V A T S Q D D C

 TACAAGTTGCCATCTCA CAGTCATCCACGGCACTGTTATGGCTGCTGTACAGC GCTTGC
 Y K F A I S Q S S T G T V M G A V I M E

 GGCTTCTACGTTGTCTTT GATCGGGCCCGAACACGAATTGGCTTGCTGTACAGC GCTTGC
 G F Y V V F D R A R K R I G F A V S A C

 CATGTG CACGATGAGTTCAAGGACGGCAGCG GTGGAAGGCCCTTTGTCACCTTG GACATG
 H V H D E F R T A A V E G P F V T L D M

 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCACCTCATGACCATA GCCTAT
 E D C G Y N I P Q T D E S T L M T I A Y

 GTCATGGCTGCCATCTGC GCCCTCTTCATG CTGCCACTCTGC CTCATGGTGTGT CAGTGG
 V M A A I C A L F M L P L C L M V C Q W

 CGCTGCCTCCGCTGCCTG CGCCAGCAGCAT GATGACTTGT GATGACATCTCC CTGCTG
 R C L R C L R Q Q H D D F A D D I S L L

 AAGTGAGGAGGCCATGG GCAGAAGATAGA GATTCCCTGGA CCACACCTCCGT GGTTCA
 K

 CTTGGTCACAAGTAGGA GACACAGATGGC ACCTGTGGCCAG AGCACCTCAGGA CCCTCC
 CCACCCACCAAATGCCCTGCGCTTGATGGA GAAGGAAAAGGC TGGCAAGGTGGG TTCCAG
 GGACTGTACCTGTAGGAA ACAGAAAAGAGA AGAAAAGAACAC TCTGCTGGCGGG AATACT
 CTTGGTCACCTCAAATTAAAGTCGGAAAT TCTGCTGCTTGA AACTTCAGCCCT GAACT
 TTGTCACCATTCTTTA AATTCTCAACC CAAAGTATTCTT CTTTTCTTAGTT TCAGAA
 GTACTGGCATCACACGCA GGTTACCTTGGC GTGTGTCCCTGT GGTACCCCTGGCA GAGAAG
 AGACCAAGCTTGTTCCC TGCTGGCAAAG TCAGTAGGAGAG GATGACAGTTT GCTATT
 TGCTT TAGAGACAGGGAC TGTATAAACAAAG CCTAACATTGGT GCAAAGATTGCC TCTTGA
 ATTAAAAAAAAAAAAAA AAAAAAAAAAAA

FIGURE 4

ATGGCCCCAGCGCTGCA CTGGCTCCTGCT ATGGGTGGGCTC GGGAAATGCTGCC TGCCCAG
 M A P A L H W L L W V G S G M L P A Q
 GGAACCCATCTCGGCAT CCGGCTGCCCT TCGCAGCGGCCCT GGCAGGGCCACC CCTGGGC
 G T H L G I R L P L R S G L A G P P L G
 CTGAGGCTCCCCGGGA GACTGACGAGGA ATCGGAGGAGCC TGGCCGGAGAGG CAGCTTT
 L R L P R E T D E E S E E P G R R G S F
 GTGGAGATGGTGGACAA CCTGAGGGAAA GTCCGGCCAGGG CTACTATGTGGA GATGACC
 V E M V D N L R G K S G Q G Y Y V E M T
 GTAGGCAGCCCCCAC A GCGCTAACAT CCTGGTGGACAC GGGCAGTAGTAA CTTTGCA
 V G S P P Q T L N I L V D T G S S N F A
 GTGGGGCTGCCAACA CCCTTCTGCA TCGCTACTACCA GAGGCAGCTGTC CAGCAC
 V G A A P H P F L H R Y Y Q R Q L S S T
 TATCGAGACCTCCGAAA GGGTGTGTATGT GCCCTACACCA GGGCAAGTGGGA GGGGGAA
 Y R D L R K G V Y V P Y T Q G K W E G E
 CTGGGCAACGACCTGGT GAGCATCCCTCA TGGCCCAACGT CACTGTGCGTGC CAACATT
 L G T D L V S I P H G P N V T V R A N I
 GCTGCCATCACTGAATC GGACAAGTCTT CATCAATGGITC CAACTGGGAGGG CATCTA
 A A I T E S D K F F I N G S N W E G I L
 GGGCTGGCTATGCTGA GATTGCCAGGCC CGACGACTCTT GGAGCCCTTC TT TGACTCC
 G L A Y A E I A R P D D S L E P F F D S
 CTGGTGAAGCAGACCCA CATTCCCACAT CTTTCCCTGCA GCTCTGGCGCTGGCTTC
 L V K Q T H I P N I F S L Q L C G A G F
 CCCCTCAACAGACCGA GGCACCTGCCCTC GGTTGGGAGGGAG CATGATCATGG TGGTATC
 P L N Q T E A L A S V G G S M I I G G I
 GACCACTCGCTATACAC GGGCAGTCTCTG GTACACACCCAT CCGGCGGGAGTG GTATTAT
 D H S L Y T G S L W Y T P I R R E W Y Y
 GAAGTGTACATTGTACG TGTGGAAATCAA TGGTCAAGATCT CAAGATGGACTG CAAGGAG
 E V I I V R V E I N G Q D L K M D C K E
 TACAACCTACGACAAGAG CATTGTGGACAG TGGGACCACCAA CCTTCGCTTGCC CAAGAAA
 Y N Y D K S I V D S G T T N L R L P K K
 GTATTGAGCTGCCGT CAAGTCCATCAA GGCAGCCTCCCT GACGGAGAAGTT CCCGGAT
 V F E A A V K S I K A A S S T E K F P D
 GGCTTTGGCTAGGGAGCAGCTGGTGTG CTGGCAAGCAGG CACGACCCCTTG GAACATT
 G F W L G E Q L V C W Q A G T T P W N I
 TTCCCAGTCATTCACT TTACCTCATGGG TGAAGTCACCAA TCAGTCCTTCCG CATCAC
 F P V I S L Y L M G E V T N Q S F R I T
 ATCCTTCCTCAGCAATA CCTACGGCCGGT GGAGGACGTGGC CACGTCCAAGA CGACTGT
 I L P Q Q Y L R P V E D V A T S Q D D C
 TACAAGTTCGCTGTCTC ACAGTCATCCAC GGGCACTGTTAT GGGAGCCGTAT CATGGAA
 Y K F A V S Q S S T G T V M G A V I M E
 GGTTTCTATGCTGCTT CGATCGAGCCCG AAAGCGAATTGG CTTTGCTGTCAG CGCTTGC
 G F Y V V F D R A R K R I G F A V S A C
 CATGTGCACGATGAGTT CAGGACGGCCGC AGTGGAAAGGTCC GTTTGTACGGC AGACATG
 H V H D E F R T A A V E G P F V T A D M
 GAAGACTGTGGCTACAA CATTCCCCAGAC AGATGAGTCAC ACTTATGACCAT AGCTTAT
 E D C G Y N I P Q T D E S T L M T I A Y
 GTCATGGCGCCATCTG CGCCCTCTTCAT GTTGCCACTCTG CCTCATGGTATG TCAGTGG
 V M A A I C A L F M L P L C L M V C Q W
 CGCTG CCTGCGTGCCT GCGCCACCAGCA CGATGACTTTGC TGATGACATCTC CCTGCTC
 R C L R C L R H Q H D D F A D D I S L L
 AAGTAAGGAGGCTCGTG GGCAGATGATGG AGACGCCCTGG ACCACATCTGGG TGGTCC
 K
 CTTGGTCACATGAGTT GGAGCTATGGAT GGTACCTGTGGC CAGAGCACCTCA GGACCC
 CACCAACCTGCCAATGC TTCTGGCGTGC AGAACAGAGAAA TCAGGCAAGCTG GATTACA
 GGGCTTGACCTGTAGG ACACAGGGAGG GAAGGAAGCAGC GTTCTGGTGGCA GGAATAT
 CCTTAGGCACCAAAAC TTGAGTTGGAAA TTTGCTGCTT GAGCTTCAGCCC TGACCC
 CTGCCCAAGCATCTTAA GAGTCTCAAC TAAAGTATTCTT TATGTCCTTCCA GAAGTAC
 TGGCGTCATACTCAGGC TACCCGGCATGT GTCCCTGTGGTA CCCTGGCAGAGA AAGGGCC
 AATCTCATCCCTGCTG GCCAAAGTCAGC AGAAGAAGGTGA AGTTTGCCAGTT GCTTTAG
 TGATAGGACTGCAGAC TCAAGCCTACAC TGGTACAAAGAC TGCCTTGTGAGA TAAACAA
 GAA

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FIGURE 5

FIGURE 6A

ATGGCTAGC ATGACTGGTGG A CAGCAAATGGT CGCGGATCCACC CAGCACGGCATC CGG
M A S M T G G Q Q M G R G S T Q H G I R
 CTGCCCTG CGCAGGCCCTG GGGGGGCCCCC CTGGGGCTGGG CTGCCCGGGAG ACC
L P L R S G L G G A P L G L R L P R E T
 GACGAAGAG CCCGAGGAGCCC GGCGGAGGGC AGCTTGTTGGAG ATGGTGGACAAC CTG
D E E P E E P G R R G S F V E M V D N L
 AGGGGCAAG TCAGGGCAGGGC TACTACGTGGAG ATGACCGTGGC AGCCCCCGCAG ACG
R G K S G Q G Y Y V E M T V G S P P Q T
 CTCAACATC CTGGTGGATACA GGCAGCAGTAAC TTTGCAGTGGT GCTGCCACCCAC CCC
L N I L V D T G S S N F A V G A A P H P
 TTCTGCAT CGCTACTACCAAG AGGCAGCTGTCC AGCACATACCGG GACCTCCGGAAG GGC
F L H R Y Y Q R Q L S S T Y R D L R K G
 GTGTATGTG CCCTACACCCAG GGCAAGTGGAA GGGGAGCTGGC ACCGACCTGGTA AGC
V Y V P Y T Q G K W E G E L G T D L V S
 ATCCCCCAT GGCCCCAACGTC ACTGTGCGTGCC AACATTGCTGCC ATCACTGAATCA GAC
I P H G P N V T V R A N I A A I T E S D
 AAGTTCTTC ATCAACGGCTCC AACTGGGAAGGC ATCCTGGGCTG GCCTATGCTGAG ATT
K F F I N G S N W E G I L G L A Y A E I
 GCCAGGCCT GACGACTCCCTG GAGCCTTCTTT GACTCTCTGGTA AAGCAGACCCAC GTT
A R P D D S L E P F F D S L V K Q T H V
 CCAAACCTC TTCTCCCTGCAG CTTTGTGGTGT GGCTTCCCCCTC AACCAAGTCTGAA GTG
P N L F S L Q L C G A G F P L N Q S E V
 CTGGCCTCT GTGGAGGGAGC ATGATCATTGG A GTATCGACCA C TCGCTGTACACA GGC
L A S V G G S M I I G G I D H S L Y T G
 AGTCTCTGG TATAACACCATC CGGCGGGACTGG TATTATGAGGTC ATCATTGTGCGG GTG
S L W Y T P I R R E W Y Y E V I I V R V
 GAGATCAAT GGACAGGATCTG AAAATGGACTGC AAGGAGTACAAC TATGACAAGAGC ATT
E I N G Q D L K M D C K E Y N Y D K S I
 GTGGACAGT GGCACCAAC CCTCGTTGCC AAGAAAAGTGTGTT GAAGCTGCAGTC AAA
V D S G T T N L R L P K K V F E A A V K
 TCCATCAAG GCAGCCTCTCC ACGGAGAAGTTC CCTGATGGTTTC TGGCTAGGAGAG CAG
S I K A A S S T E K F P D G F W L G E Q
 CTGGTGTGC TGGCAAGCAGGC ACCACCCCTGG AACATTTCCAGTCATCTCACTC TAC
L V C W Q A G T T P W N I F P V I S L Y
 CTAATGGGT GAGGTACCAAC CAGTCCTCCGC ATCACCATCCTT CCGCAGCAATAC CTG
L M G E V T N Q S F R I T I L P Q Q Y L
 CGGCCAGTGG AAGATGTGGCA CGTCCAAGACG ACTGTTACAAGT TTGCCATCTCAC AG

FIGURE 6B

R P V E D V A T S Q D D C Y K F A I S Q
TCATCCACGG GCACTGTTATGG GAGCTGTTATCA TGGAGGGCTTCT ACCTTGCTTTGAT
S S T G T V M G A V I M E G F Y V V F D
CGGGCCCCGAA AACGAATTGGCT TTGCTGTCAGCG CTTGCCATGTGC ACGATGAGTTCA GG
R A R K R I G F A V S A C H V H D E F R
ACGGCAGCGG TGGAAAGGCCCTT TTGTCACCTTG GACATGGAAGACT GTGGCTACAACA TT
T A A V E G P F V T L D M E D C G Y N I
CCACAGACAG ATGAGTCATGA
P Q T D E S *

FIGURE 7A

ATGGCTAGC ATGACTGGTGG A CAGCAAATGGGT CGCGGATCGATG ACTATCTCTGAC TCT
M A S M T G G Q Q M G R G S M T I S D S
 CCGCGTGA CAGGACGGATCC ACCCAGCACGGC ATCCGGCTGCC CTGCGCAGCGGC CTG
P R E Q D G S T Q H G I R L P L R S G L
 GGGGGCGCC CCCCTGGGGCTG CGGCTGCCCCGG GAGACCGACGAA GAGCCCGAGGAG CCC
G G A P L G L R L P R E T D E E P E E P
 GGCGGGAGG GGCAGCTTG TG GAGATGGTGGAC AACCTGAGGGGC AAGTCGGGCAG GGC
G R R G S F V E M V D N L R G K S G Q G
 TACTACGTG GAGATGACCGTG GGCAGCCCCCG CAGACGCTCAAC ATCCTGGTGGAT ACA
Y Y V E M T V G S P P Q T L N I L V D T
 GGCAGCAGT AACCTTGCA GTG GGTGCTGCC CACCCCTTCC TG CATCGCTACTAC CAG
G S S N F A V G A A P H P F L H R Y Y Q
 AGGCAGCTG TCCAGCACATAC CGGGACCTCCGG AAGGGCGTGTAT GTGCCCTACACC CAG
R Q L S S T Y R D L R K G V Y V P Y T Q
 GGCAAGTGG GAAGGGGAGCTG GGCACCGACCTG GTAAGCATCCCC CATGGCCCCAAC GTC
G K W E G E L G T D L V S I P H G P N V
 ACTGTGCGT GCCAACATTGCT GCCATCACTGAA TCAGACAAGTT TTCATCAACGGC TCC
T V R A N I A A I T E S D K F F I N G S
 AACTGGGAA GGCATCCTGGGG CTGGCTATGCT GAGATTGCCAGG CCTGACGACTCC CTG
N W E G I L G L A Y A E I A R P D D S L
 GAGCCTTTC TTTGACTCTCTG GTAAAGCAGACC CACGTTCCAAC CTCTTCTCCCTG CAG
E P F F D S L V K Q T H V P N L F S L Q
 CTTTGTGGT GCTGGCTTCCCC CTCACCCAGTCT GAAGTGCTGGCC TCTGTCGGAGGG AGC
L C G A G F P L N Q S E V L A S V G G S
 ATGATCATT GGAGGTATCGAC CACTCGCTGTAC ACAGGCAGTC TGGTATAACACCC ATC
M I I G G I D H S L Y T G S L W Y T P I
 CGCGGGAG TGGTATTATGAG GTCATCATTGTG CGGGTGGAGATC AATGGACAGGAT CTG
R R E W Y Y E V I I V R V E I N G Q D L
 AAAATGGAC TGCAAGGAGTAC AACTATGACAAG AGCATTGGAC AGTGGCACCAAC AAC
K M D C K E Y N Y D K S I V D S G T T N
 CTTCGTTTG CCCAAGAAAGTG TTTGAAGCTGCA GTCAAATCCATC AAGGCAGCCTCC TCC
L R L P K K V F E A A V K S I K A A S S
 ACGGAGAAG TTCCCTGATGGT TTCTGGCTAGGA GAGCAGCTGGTG TGCTGGCAAGCA GGC
T E K F P D G F W L G E Q L V C W Q A G
 ACCACCCCTT GGAACATTTCC CAGTCATCTCACTCTACCTAATGG GTGAGGTTACCA AC
T T P W N I F P V I S L Y L M G E V T N

FIGURE 7B

CAGTCCTTCC GCATCACCATCC TTCCGCAGCAAT ACCTGCGGCCAG TGGAAGATGTGG CC
Q S F R I T I L P Q Q Y L R P V E D V A

ACGTCCCAAG ACGACTGTTACA AGTTGCCATCT CACAGTCATCCA CGGGCACTGTTA TG
T S Q D D C Y K F A I S Q S S T G T V M

GGAGCTGTTA TCATGGAGGGCT TCTACGTTGTCT TTGATCGGGCCC GAAAACGAATTGGC
G A V I M E G F Y V V F D R A R K R I G

TTTGCTGTCA GCGCTTGCATG TGCAAGATGAGT TCAGGACGGCAG CGGTGGAAGGCC CT
F A V S A C H V H D E F R T A A V E G P

TTTGTACCT TGGACATGGAAG ACTGTGGCTACA ACATTCCACAGA CAGATGAGTCAT GA
F V T L D M E D C G Y N I P Q T D E S *

FIGURE 8A

ATGACTCAGCATGG TATTCGTCTGCC ACTGCGTAGCGG TCTGGGTGGTGC TCCACTGGGT
 M T Q H G I R L P L R S G L G G A P L G -

 CTGGCTCTGCCCG GGAGACCGACGA AGAGCCCGAGGA GCCCCGCCGGAG GGGCAGCTTT
 L R L P R E T D E E P E E P G R R G S F -

 GTGGAGATGGTGG CAACCTGAGGGG CAAGTCGGGCAGGGCTACTACGT GGAGATGACC
 V E M V D N L R G K S G Q G Y Y V E M T -

 GTGGGCAGCCCCC GCAGACGCTCAA CATCTGGTGG A TACAGGCAGCAG TAACTTGCA
 V G S P P Q T L N I L V D T G S S N F A -

 GTGGGTGCTGCC CCACCCCTTCCT GCATCGCTACTA CCAGAGGCAGCT GTCCAGCACA
 V G A A P H P F L H R Y Y Q R Q L S S T -

 TACCGGGACCTCCG GAAGGGCGTGT A TGTCGCCTACAC CCAGGGCAAGTG GGAAGGGGAG
 Y R D L R K G V Y V P Y T Q G K W E G E -

 CTGGGCACCGACCT GGTAAGCATCCC CCATGGCCCAA CGTCACTGTGCG TGCCAACATT
 L G T D L V S I P H G P N V T V R A N I -

 GCTGCCATCACTGA ATCAGACAAGTT CTTCATCACGG CTCCAACGGG AGGCATCCG
 A A I T E S D K F F I N G S N W E G I L -

 GGGCTGGCTATGC TGAGATTGCCAG GCCTGACGACTC CCTGGAGCCTTT CTTGACTCT
 G L A Y A E I A R P D D S L E P F F D S

 CTGGTAAAGCAGAC CCACGTTCCCAA CCTCTTCTCCCT GCAGCTTGTTGTGG TGCTGGCTTC
 L V K Q T H V P N L F S L Q L C G A G F -

 CCCCTCAACCAGTC TGAAAGTGTGGC CTCTGTCGGAGG GAGCATGATCAT TGGAGGTATC
 P L N Q S E V L A S V G G S M I I G G I -

 GACCACTCGCTGT A CACAGGCAGTCT CTGGTATAACACC CATCCGGGGGAGTGGTATTAT
 D H S L Y T G S L W Y T P I R R E W Y Y -

 GAGGTCACTATTGT GCGGGTGGAGAT CAATGGACAGGA TCTGAAAATGGA CTGCAAGGAG
 E V I I V R V E I N G Q D L K M D C K E

 TACAACTATGACAA GAGCATTGTGG A CAGTGGCACCAC CAACCTCGTTT GCCCAAGAAA
 Y N Y D K S I V D S G T T N L R L P K K -

 GTTTGAAGCTGC AGTCAAATCCAT CAAGGCAGCCTC CTCCACGGAGAA GTTCCCTGAT
 V F E A A V K S I K A A S S T E K F P D -

 GGTTTCTGGCTAGG AGAGCAGCTGGT GTGCTGGCAAGC AGGCACCACCC TTGGAACATT
 G F W L G E Q L V C W Q A G T T P W N I -

 TTCCCAGTCATCTC ACTCTACCTAAT GGGTGAGGTAC CAACCACTCCTT TCGCATCACC
 F P V I S L Y L M G E V T N Q S F R I T -

 ATCCTCCGAGCA ATACCTGGGGCC AGTGGAAAGATGT GGCCACGTCCC AGACGACTGT
 I L P Q Q Y L R P V E D V A T S Q D D C -

FIGURE 8B

TACAAGTTGCCAT CTCACAGTCATC CACGGGCACTGT TATGGGAGCTGT TATCATGGAG
Y K F A I S Q S S T G T V M G A V I M E -

GGCTTCTACGTTGT CTTTGATCGGGC CCGAAAACGAAT TGGCTTGCTGT CAGCGCTTGC
G F Y V V F D R A R K R I G F A V S A C -

CATTAG
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FIGURE 9

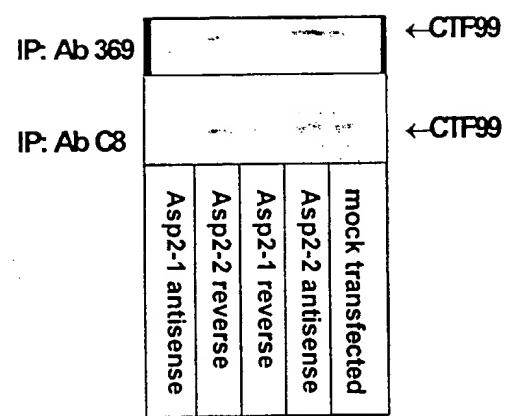


FIGURE 10

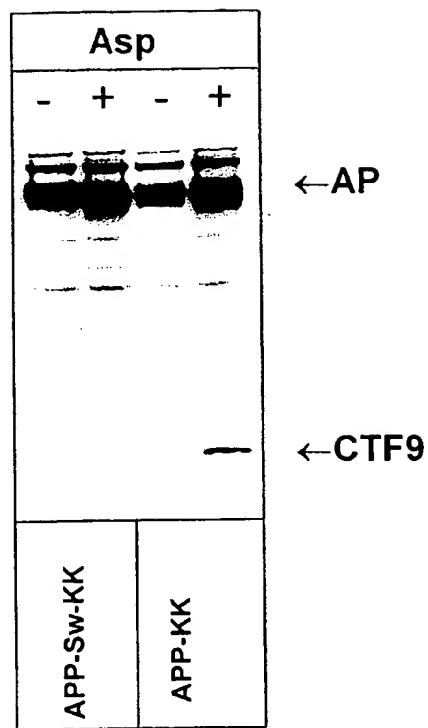


FIGURE 11

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DES

FIGURE 12

MAQALPWLLLWMGAGVLP AHLPAHGTQHGIRLPLRSGLGGAPLGLRLPRETDEE
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YTPIRREWYYEVII VRVEINGQDLKMDCKE NYDKSIVD SGT TNLRLPKK
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SEQUENCE LISTING

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Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
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<211> 476

<212> PRT

<213> Homo sapiens

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- 7 -

Gly Leu Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
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 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
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 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
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 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
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 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
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 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Leu Cys Gly
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 Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly
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 Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu
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 Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val
 225 230 235 240
 Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr
 245 250 255
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 Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser
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 Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser
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 Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile
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 340 345 350
 Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val
 355 360 365

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Ile	Ala	Tyr	Val	Met	Ala	Ala	Ile	Cys	Ala	Leu	Phe	Met	Leu	Pro	Leu
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Cys	Leu	Met	Val	Cys	Gln	Trp	Arg	Cys	Leu	Arg	Cys	Leu	Arg	Gln	Gln
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- 9 -

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 50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
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Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
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Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
 115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
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Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
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Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
 180 185 190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Ile Pro
 195 200 205

Asn Ile Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
 210 215 220

Thr Glu Ala Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
 225 230 235 240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
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Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
 260 265 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
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Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
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- 10 -

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
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Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
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Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
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Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
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Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
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Val Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
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Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
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Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
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Gly Pro Phe Val Thr Ala Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
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Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
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Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
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Ile Ser Leu Leu Lys
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<210> 9
<211> 2088
<212> DNA
<213> *Homo sapiens*

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- 11 -

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<211> 695

<212> PRT

<213> Homo sapiens

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25

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Gln	Ile	Ala	Met	Phe	Cys	Gly	Arg	Leu	Asn	Met	His	Met	Asn	Val	Gln

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55

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Thr	Lys	Glu	Gly	Ile	Leu	Gln	Tyr	Cys	Gln	Glu	Val	Tyr	Pro	Glu	Leu

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90

95

Trp	Cys	Lys	Arg	Gly	Arg	Lys	Gln	Cys	Lys	Thr	His	Pro	His	Phe	Val

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105

110

Ile	Pro	Tyr	Arg	Cys	Leu	Val	Gly	Glu	Phe	Val	Ser	Asp	Ala	Leu	Leu

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120

125

Val	Pro	Asp	Lys	Cys	Lys	Phe	Leu	His	Gln	Glu	Arg	Met	Asp	Val	Cys

130

135

140

Glu	Thr	His	Leu	His	Trp	His	Thr	Val	Ala	Lys	Glu	Thr	Cys	Ser	Glu

145

150

155

160

Lys	Ser	Thr	Asn	Leu	His	Asp	Tyr	Gly	Met	Leu	Leu	Pro	Cys	Gly	Ile

165

170

175

Asp	Lys	Phe	Arg	Gly	Val	Glu	Phe	Val	Cys	Cys	Pro	Leu	Ala	Glu	Glu

180

185

190

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195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210 215 220

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225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
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Ala Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
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Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
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Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
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Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
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Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
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Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
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Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
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Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe
405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
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Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala
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Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
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465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
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500 505 510

- 13 -

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
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Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
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Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
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Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
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Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
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His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Val Val Ile Ala Thr Val
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645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
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<211> 2088

<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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			20					25				30			

Gln	Ile	Ala	Met	Phe	Cys	Gly	Arg	Leu	Asn	Met	His	Met	Asn	Val	Gln
			35				40				45				

Asn	Gly	Lys	Trp	Asp	Ser	Asp	Pro	Ser	Gly	Thr	Lys	Thr	Cys	Ile	Asp
			50				55				60				

Thr	Lys	Glu	Gly	Ile	Leu	Gln	Tyr	Cys	Gln	Glu	Val	Tyr	Pro	Glu	Leu
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Gln	Ile	Thr	Asn	Val	Val	Glu	Ala	Asn	Gln	Pro	Val	Thr	Ile	Gln	Asn
				85				90				95			

Trp	Cys	Lys	Arg	Gly	Arg	Lys	Gln	Cys	Lys	Thr	His	Pro	His	Phe	Val
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Ile	Pro	Tyr	Arg	Cys	Leu	Val	Gly	Glu	Phe	Val	Ser	Asp	Ala	Leu	Leu
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Val	Pro	Asp	Lys	Cys	Lys	Phe	Leu	His	Gln	Glu	Arg	Met	Asp	Val	Cys
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Glu	Thr	His	Leu	His	Trp	His	Thr	Val	Ala	Lys	Glu	Thr	Cys	Ser	Glu
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Asp	Lys	Phe	Arg	Gly	Val	Glu	Phe	Val	Cys	Cys	Pro	Leu	Ala	Glu	Glu
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Ser	Asp	Asn	Val	Asp	Ser	Ala	Asp	Ala	Glu	Glu	Asp	Asp	Ser	Asp	Val
			195				200				205				

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Val	Val	Glu	Val	Ala	Glu	Glu	Glu	Val	Ala	Glu	Val	Glu	Glu	Glu	
225					230				235			240			
Glu	Ala	Asp	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Gly	Asp	Glu	Val	Glu	Glu
		245				250			255						
Glu	Ala	Glu	Glu	Pro	Tyr	Glu	Glu	Ala	Thr	Glu	Arg	Thr	Thr	Ser	Ile
		260				265			270						
Ala	Thr	Glu	Ser	Val	Glu	Glu	Val	Val	Arg						
	275				280				285						
Val	Pro	Thr	Thr	Ala	Ala	Ser	Thr	Pro	Asp	Ala	Val	Asp	Lys	Tyr	Leu
	290					295				300					
Glu	Thr	Pro	Gly	Asp	Glu	Asn	Glu	His	Ala	His	Phe	Gln	Lys	Ala	Lys
	305				310			315			320				
Glu	Arg	Leu	Glu	Ala	Lys	His	Arg	Glu	Arg	Met	Ser	Gln	Val	Met	Arg
	325					330			335						
Glu	Trp	Glu	Glu	Ala	Glu	Arg	Gln	Ala	Lys	Asn	Leu	Pro	Lys	Ala	Asp
	340					345			350						
Lys	Lys	Ala	Val	Ile	Gln	His	Phe	Gln	Glu	Lys	Val	Glu	Ser	Leu	Glu
	355					360			365						
Gln	Glu	Ala	Ala	Asn	Glu	Arg	Gln	Gln	Leu	Val	Glu	Thr	His	Met	Ala
	370					375			380						
Arg	Val	Glu	Ala	Met	Leu	Asn	Asp	Arg	Arg	Arg	Leu	Ala	Leu	Glu	Asn
	385					390			395			400			
Tyr	Ile	Thr	Ala	Leu	Gln	Ala	Val	Pro	Pro	Arg	Pro	Arg	His	Val	Phe
	405						410			415					
Asn	Met	Leu	Lys	Lys	Tyr	Val	Arg	Ala	Glu	Gln	Lys	Asp	Arg	Gln	His
	420						425			430					
Thr	Leu	Lys	His	Phe	Glu	His	Val	Arg	Met	Val	Asp	Pro	Lys	Lys	Ala
	435						440			445					
Ala	Gln	Ile	Arg	Ser	Gln	Val	Met	Thr	His	Leu	Arg	Val	Ile	Tyr	Glu
	450					455			460						
Arg	Met	Asn	Gln	Ser	Leu	Ser	Leu	Leu	Tyr	Asn	Val	Pro	Ala	Val	Ala
	465					470			475			480			
Glu	Glu	Ile	Gln	Asp	Glu	Val	Asp	Glu	Leu	Leu	Gln	Lys	Glu	Gln	Asn
	485					490			495						
Tyr	Ser	Asp	Asp	Val	Leu	Ala	Asn	Met	Ile	Ser	Glu	Pro	Arg	Ile	Ser
	500						505			510					
Tyr	Gly	Asn	Asp	Ala	Leu	Met	Pro	Ser	Leu	Thr	Glu	Thr	Lys	Thr	Thr
	515					520			525						
Val	Glu	Leu	Leu	Pro	Val	Asn	Gly	Glu	Phe	Ser	Leu	Asp	Asp	Leu	Gln
	530					535			540						

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Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn		
545	550	555
Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr		
565	570	575
Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser		
580	585	590
Glu Val Asn Leu Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val		
595	600	605
His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys		
610	615	620
Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val		
625	630	635
Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile		
645	650	655
His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg		
660	665	670
His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys		
675	680	685
Phe Phe Glu Gln Met Gln Asn		
690	695	

<210> 13
<211> 2088
<212> DNA
<213> Homo sapiens

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ctgaacatgc acatgaatgt ccagaatggg aagtggatt cagatccatc agggaccaaa 180
accgtcattt ataccaagga aggcatcctg cagtattgcc aagaagtcta ccctgaactg 240
cagatcacca atgtggtaga agccaaccaa ccagtgcacca tccagaactg gtcaagcgg 300
ggccgcaagc agtgcacagac ccatccccac ttgtgattt cctaccgctg cttatgttgt 360
gagtttgtaa gtgtatgcct tctcggttct gacaagtgc aattcttaca ccaggagagg 420
atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccääagagac atgcagttag 480
aagagtacca acttgcatga ctacggcatg ttgctgccc gcggaatttg caagttccga 540
gggttagagt ttgtgttgtt cccactggct gaagaaaagtg acaatgttgaa ttctgtgtat 600
gcggaggagg atgactcgga tgcgttgg ggcggaggcag acacagacta tgcagatggg 660
agttaagaca aagttagtaga agtagcagag gaggaaagaatg tggctgagggt ggaagaagaa 720
gaagccgtatg atgacggaggat cgatggatgtt ggtgtatgg tagaggaaga ggctgaggaa 780
ccctacgaag aagccacaga gagaaccacc agattgcaccc ccaccacacc caccaccaca 840
gagtcgttgtt aagagggtgtt tcgagttctt acaacagcag ccagtacccc tgatgccgtt 900
gacaagtata tcgagacacc tggggatgtt aatgaacatg cccatccc gaaagccaaa 960
gagaggctt aggccaaagca ccggagagaga atgtcccagg tcatgagaga atggaaagag 1020
gcagaacgtc aagcaaaagaa cttgcctaaa gctgataaga aggcatgtt ccacgtttc 1080
caggagaaag tggaaatctt ggaacaggaa gcagccaaacg agagacacgca gctgggtgg 1140
acacacatgg ccagagtggaa agccatgttc aatgaccgc gccgcctggc cctggagaac 1200
tacatcaccg ctctgcaggc tggcttccctt cggcctcgatc acgtgttcaa tatgttaaag 1260
aagtatgtcc ggcgcagaaca gaaggacaga cagcacaccc taaagcattt cgagcatgtg 1320
cgcatgggtt atcccaagaa agccgctcag atccgggtccc aggttatgac acacccctgt 1380
gtgtttatg agcgcatgaa tcagttctc tccctgtctt acaacgtgcc tgcagtggcc 1440
gaggagatttcc agatgttgc tgcgttgc ttcagaaag agcaaaaactt ttcagatgac 1500
gtcttggcca acatgatttac tgaaccaagg atcagttacg gaaacgtgc tctcatgcca 1560

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tctttgaccg aaacgaaaac caccgtggag ctccccc tgaatggaga gttcagcctg 1620
 gacgatctcc agccgtggca ttctttggg gctgactctg tgccagccaa cacagaaaac 1680
 gaagttgagc ctgttgatgc ccgcctgct gccgaccgag gactgaccac tcgaccagg 1740
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 cgacatgact cagggatcatca caaaaattgg tttctttgc agaagatgtg 1860
 ggttcaaaaca aaggtaaat cattggactc atggggcg gtgtgtcat agcgacagt 1920
 atcttcatca ccttgggtat gctgaagaag aaacagtaca catccattca tcatgggtg 1980
 gtggagggtg acggccgtgt cacccccagag gagcgcacc tgcggcaat gcagcagaac 2040
 ggctacgaaa atccaaccta caagttttt gagcagatgc agaactag 2088

<210> 14
 <211> 695
 <212> PRT
 <213> Homo sapiens

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Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
 35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
 50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
 65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
 85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
 100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
 115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
 130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
 145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
 165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
 180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
 195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
 210 215 220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
 225 230 235 240

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Glu Ala Asp Asp Asp	Glu Asp Asp Glu	Asp Gly Asp Glu Val	Glu Glu
245	250		255
Glu Ala Glu Glu Pro Tyr	Glu Glu Ala Thr	Glu Arg Thr Thr Ser Ile	
260	265	270	
Ala Thr Thr Thr Thr Thr	Glu Ser Val	Glu Val Val Arg	
275	280	285	
Val Pro Thr Thr Ala Ala	Ser Thr Pro Asp Ala Val	Asp Lys Tyr Leu	
290	295	300	
Glu Thr Pro Gly Asp	Glu Asn Glu His Ala His	Phe Gln Lys Ala Lys	
305	310	315	320
Glu Arg Leu Glu Ala Lys	His Arg Glu Arg Met	Ser Gln Val Met Arg	
325	330	335	
Glu Trp Glu Glu Ala Glu Arg	Gln Ala Lys Asn Leu Pro	Lys Ala Asp	
340	345	350	
Lys Lys Ala Val Ile Gln	His Phe Gln Glu Lys Val	Glu Ser Leu Glu	
355	360	365	
Gln Glu Ala Ala Asn Glu Arg	Gln Gln Leu Val Glu	Thr His Met Ala	
370	375	380	
Arg Val Glu Ala Met Leu Asn Asp Arg	Arg Arg Arg Leu Ala	Leu Glu Asn	
385	390	395	400
Tyr Ile Thr Ala Leu Gln	Ala Val Pro Pro Arg	Pro Arg His Val Phe	
405	410	415	
Asn Met Leu Lys Lys Tyr Val	Arg Ala Glu Gln Lys Asp	Arg Gln His	
420	425	430	
Thr Leu Lys His Phe Glu His	Val Arg Met Val Asp	Pro Lys Ala	
435	440	445	
Ala Gln Ile Arg Ser Gln Val	Met Thr His Leu Arg	Val Ile Tyr Glu	
450	455	460	
Arg Met Asn Gln Ser Leu	Ser Leu Leu Tyr Asn Val	Pro Ala Val Ala	
465	470	475	480
Glu Glu Ile Gln Asp	Glu Val Asp Glu	Leu Gln Lys Glu Gln Asn	
485	490	495	
Tyr Ser Asp Asp Val Leu	Ala Asn Met Ile Ser	Glu Pro Arg Ile Ser	
500	505	510	
Tyr Gly Asn Asp Ala Leu	Met Pro Ser Leu Thr	Glu Thr Lys Thr Thr	
515	520	525	
Val Glu Leu Leu Pro Val	Asn Gly Glu Phe Ser	Leu Asp Asp Leu Gln	
530	535	540	
Pro Trp His Ser Phe Gly	Ala Asp Ser Val Pro	Ala Asn Thr Glu Asn	
545	550	555	560

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Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Val Ile Ala Thr Val
625 630 635 640

Ile Phe Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
675 680 685

Phe Phe Glu Gln Met Gln Asn
690 695

<210> 15
<211> 2094
<212> DNA
<213> *Homo sapiens*

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ctgaacatgc	acatgaatgt	cc	agaatggg	aagtgggatt	cagatccat	agggacaaa	180	
acctgcattg	ataccaaagg	agg	catecttg	cagtatgcc	aagaagtcta	ccctgaaact	240	
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ggccgcaagc	agtgcagac	ccatccccac	tttgtgattc	ccttaccgcgt	cttagttgg	360		
gagtttgtaa	gtgtgcct	tctcggtcct	gacaagtgc	aattcttaca	ccaggagagg	420		
atggatgttt	gcgaaactca	tcttca	cacaccgtcg	ccaaagagac	atgcagttag	480		
aagagtacca	acttgc	atga	ctacggcatg	ttgctgcct	gccaatttg	caagttccga	540	
ggggtagagt	tttgtgtt	g	ccactggct	gaagaaagt	acaatgttg	ttctgctgt	600	
gcggaggagg	atgactcg	tg	tctgggt	ggcggagcag	acacagacta	tgcagatgg	660	
agtgaagaca	aagttagta	ag	tagcagac	gaggaaga	tggctgagg	ggaagaagaa	720	
gaagccgtat	atgacgag	cgat	gaggat	gttgcgagg	tagaggaa	ggctgaggaa	780	
ccctacgaa	aaggccac	gaga	accacc	acgattgcca	ccaccac	caccacca	840	
gagtctgttt	aaagggtt	tc	gatgttct	acaacacg	ccatgtcccc	tgatgcgtt	900	
gacaagtatc	tcgagacacc	tggg	gatgaa	aatgaacat	cccatattcc	gaaagccaaa	960	
gagaggctt	aggcca	ccg	agagaga	atgtcc	cagg	tcatgagaga	atgggaagag	1020
gcagaacgtc	aagcaaagaa	cttgcctaa	aa	gtgataa	aggcagtt	ccagcattt	ccagcattt	1080
caggagaaag	tggatctt	gga	acaggaa	gcagccaa	cg	agagacagca	gtctggggag	1140
acaacatgg	ccagatgg	ag	ccatgct	aatgacc	cc	ccgcctggc	cctggagaac	1200
tacatcaccg	ctctgcaggc	tgtt	ccctct	cggcctcg	tc	acgtgttcaa	tatgctaaag	1260
aagtatgtcc	gwgca	aa	aggacaga	cagcac	ccc	taaagcat	cgagcatgt	1320
cgcatgggg	atcccaagaa	ag	ccgtcg	atccgg	ttcc	ttttgtac	acacccctgt	1380
gtgatttatg	agcgc	atgaa	tcgttctc	tccctgtct	acaacgt	cc	tgcatggcc	1440
gaggagatc	aggatgaa	tgatg	actggct	ttt	caga	aaacta	ttcagatgac	1500
gtcttggcca	acatgattag	tga	accaagg	atcagtt	acg	gaaacgat	tctcatgcca	1560
tctttgaccg	aaacgaaaac	cac	cggtggag	ctccttcc	tga	aatggaga	gttcagcctg	1620
gacgatctcc	agccgtgg	tt	tttttggg	gctgact	tc	tgccagccaa	cacagaaaaac	1680

- 20 -

gaagttgagc ctgttgatgc ccggccctgct gccgaccgag gactgaccac tcgaccagg 1740
 tctgggttga caaatatcaa gacggaggag atctctgaag tgaagatgga tgcagaattc 1800
 cgacatgact caggatatga agttcatcat caaaaattgg tggtcttgc agaaagatgtg 1860
 ggtaaaaca aaggtaaat cattgactc atgggtggcg gtgttgcata agcagactg 1920
 atcgtcatca ctttgtat gctgaagaag aaacagtaca catccattca tcattgtgtg 1980
 gtggagggtg acggcgctgt caccccgag gagcgcacc tgcataaagat gcagcagaac 2040
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<210> 16
 <211> 697
 <212> PRT
 <213> Homo sapiens

<400> 16
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Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
 20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
 35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
 50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
 65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
 85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
 100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
 115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
 130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
 145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
 165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
 180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
 195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
 210 215 220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
 225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
 245 250 255

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Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile		
260	265	270
Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg		
275	280	285
Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu		
290	295	300
Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys		
305	310	315
Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg		
325	330	335
Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp		
340	345	350
Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu		
355	360	365
Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala		
370	375	380
Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn		
385	390	395
Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe		
405	410	415
Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His		
420	425	430
Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala		
435	440	445
Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu		
450	455	460
Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala		
465	470	475
Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn		
485	490	495
Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser		
500	505	510
Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr		
515	520	525
Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln		
530	535	540
Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn		
545	550	555
Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr		
565	570	575

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Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Val Ile Ala Thr Val
625 630 635 640

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
660 . 665 . 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
675 680 685

Phe Phe Glu Gln Met Gln Asn Lys Lys
690 695

<210> 17

<211> 2094

<212> DNA

<213> Homo sapiens

<400> 17

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 atcgatca cttgggtat gctgaagaag aaacagataca catccatca tcatggtgtg 1980
 gtggaggtt acggcgctgt cacccccagag gagcgccacc tgcacaaat gcagcagaac 2040
 ggctacaaa atccaaccta caagttctt gagcagatgc agaacaagaa gtag 2094

<210> 18
 <211> 697
 <212> PRT
 <213> Homo sapiens

<400> 18
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 20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
 35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
 50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
 65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
 85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
 100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
 115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
 130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
 145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
 165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
 180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
 195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
 210 215 220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
 225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
 245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
 260 265 270

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Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg			
275	280	285	
Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu			
290	295	300	
Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys			
305	310	315	320
Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg			
325	330	335	
Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp			
340	345	350	
Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu			
355	360	365	
Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala			
370	375	380	
Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn			
385	390	395	400
Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe			
405	410	415	
Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His			
420	425	430	
Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala			
435	440	445	
Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu			
450	455	460	
Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala			
465	470	475	480
Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn			
485	490	495	
Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser			
500	505	510	
Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr			
515	520	525	
Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln			
530	535	540	
Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn			
545	550	555	560
Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr			
565	570	575	
Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser			
580	585	590	

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<210> 19  
<211> 2094  
<212> DNA  
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<210> 20
<211> 697
<212> PRT
<213> Homo sapiens

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Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
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Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
35 40 45
Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
50 55 60
Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65 70 75 80
Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
85 90 95
Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100 105 110
Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125
Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130 135 140
Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160
Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
165 170 175
Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
180 185 190
Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195 200 205
Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210 215 220
Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225 230 235 240
Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
245 250 255
Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
260 265 270
Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
275 280 285

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Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe
405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala
435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala
465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
610 615 620

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Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Val Ile Ala Thr Val
625 630 635 640

Ile Phe Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
675 680 685

Phe Phe Glu Gln Met Gln Asn Lys Lys
690 695

<210> 21

<211> 1341

<212> DNA

<213> Homo sapiens

<400> 21

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gacaaaggac ccqaggagcc cggccggagg ggcagctttg tggagatgtt ggacaacctg 180
agggcaagt cggggcagggt ctactacgtt gagatgaccg tggcagcccc cccgcagacg 240
ctcaacatcc tggtgatac aggacgcgtt aactttgcgtt tgggtctgc cccccacccc 300
ttcctgcatac gtactaccca gaggcagctg tccagcacat accgggaccc cggaaagggt 360
gtgtatgttc cttacacccca gggcaagtgg gaaggggagc tggcaccga cctgtaagc 420
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tcatccacgg gcaactgttat gggagctgtt atcatgggg gcttcaatgtt tgcgtttgtt 1200
cgggcccgaa aacgaattgg ctttgcgttc agcgtttccatg atgtgcacga tgagttcagg 1260
acggcagcgg tggaaaggccc ttttgcacc ttggacatgg aagactgtgg ctacaacattt 1320
ccacagacatg atgatgttcatg a 1341

<210> 22

<211> 446

<212> PRT

<213> Homo sapiens

<400> 22

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Thr Gln
1 5 10 15

His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala Pro Leu
20 25 30

Gly Leu Arg Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly
35 40 45

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Arg	Arg	Gly	Ser	Phe	Val	Glu	Met	Val	Asp	Asn	Leu	Arg	Gly	Lys	Ser
50						55					60				
Gly	Gln	Gly	Tyr	Tyr	Val	Glu	Met	Thr	Val	Gly	Ser	Pro	Pro	Gln	Thr
65					70				75					80	
Leu	Asn	Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Gly	Ala
					85				90				95		
Ala	Pro	His	Pro	Phe	Leu	His	Arg	Tyr	Tyr	Gln	Arg	Gln	Leu	Ser	Ser
					100			105			110				
Thr	Tyr	Arg	Asp	Leu	Arg	Lys	Gly	Val	Tyr	Val	Pro	Tyr	Thr	Gln	Gly
					115			120			125				
Lys	Trp	Glu	Gly	Glu	Leu	Gly	Thr	Asp	Leu	Val	Ser	Ile	Pro	His	Gly
					130			135			140				
Pro	Asn	Val	Thr	Val	Arg	Ala	Asn	Ile	Ala	Ala	Ile	Thr	Glu	Ser	Asp
					145			150			155			160	
Lys	Phe	Phe	Ile	Asn	Gly	Ser	Asn	Trp	Glu	Gly	Ile	Leu	Gly	Leu	Ala
					165				170			175			
Tyr	Ala	Glu	Ile	Ala	Arg	Pro	Asp	Asp	Ser	Leu	Glu	Pro	Phe	Asp	
					180				185			190			
Ser	Leu	Val	Lys	Gln	Thr	His	Val	Pro	Asn	Leu	Phe	Ser	Leu	His	Leu
					195			200			205				
Cys	Gly	Ala	Gly	Phe	Pro	Leu	Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val
					210			215			220				
Gly	Gly	Ser	Met	Ile	Ile	Gly	Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly
					225			230			235			240	
Ser	Leu	Trp	Tyr	Thr	Pro	Ile	Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile
					245				250			255			
Ile	Val	Arg	Val	Glu	Ile	Asn	Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys
					260			265			270				
Glu	Tyr	Asn	Tyr	Asp	Lys	Ser	Ile	Val	Asp	Ser	Gly	Thr	Thr	Asn	Leu
					275			280			285				
Arg	Leu	Pro	Lys	Lys	Val	Phe	Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala
					290			295			300				
Ala	Ser	Ser	Thr	Glu	Lys	Phe	Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln
					305			310			315			320	
Leu	Val	Cys	Trp	Gln	Ala	Gly	Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val
					325				330			335			
Ile	Ser	Leu	Tyr	Leu	Met	Gly	Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile
					340			345			350				
Thr	Ile	Leu	Pro	Gln	Gln	Tyr	Leu	Arg	Pro	Val	Glu	Asp	Val	Ala	Thr
					355			360			365				
Ser	Gln	Asp	Asp	Cys	Tyr	Lys	Phe	Ala	Ile	Ser	Gln	Ser	Ser	Thr	Gly
					370			375			380				

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Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp
385 390 395 400

Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His
405 410 415

Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp
420 425 430

Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser
435 440 445

<210> 23

<211> 1380

<212> DNA

<213> Homo sapiens

<400> 23

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ggggcgcccc ccctggggct gcggctgccc cgggagaccg acgaagagcc cgaggagccc 180
ggccggaggg gcagctttgt ggagatgggt gacaacctga gggcaagtc ggggcaggcc 240
tactacgtgg agatgaccgt gggcagecccc cccgacacgc tcaacatctt ggtggataca 300
ggcagcagta actttgcagt ggggtgcgtcc ccccaacctt tcctgcacatcg ctactaccag 360
aggcagctgt ccagcacata cccggacactc cggaaagggtg tttatgtgcc ctacacccag 420
ggcaagtggg aaggggaggtt gggcacccgc ctggtaagca tcccccatgg ccccaacgtc 480
actgtgcgtg ccaacattgc tgccatcaat gaatcagaca agtttttcat caacggctcc 540
aactggaaag gcatcctggg gttggcttat gttggatgtt ccaggctga cgactccctg 600
gagctttct ttgactctt ggttaaaggat accacacgttcc ccaacctttt ctccctgcac 660
ctttgtggtg ctggcttccc cctcaaccag tctgaagtgc tggcctctgtt cggagggagc 720
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aaaatggact gcaaggagta caactatgac aagacattt tggacagttt caccaccaac 900
cttcgtttgc ccaagaaatg gtttgaagct gcatcaaat ccatcaaggc agcctctcc 960
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ggagctgtta tcatgggggg cttctacgtt gtctttgtatc gggccggaaa acgaattggc 1260
tttgcgttca ggccttgcca tttgcacatgtt gatgttccatc cggcagccgtt ggaaggccct 1320
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<210> 24

<211> 459

<212> PRT

<213> Homo sapiens

<400> 24

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Met Thr
1 5 10 15

Ile Ser Asp Ser Pro Arg Glu Gln Asp Gly Ser Thr Gln His Gly Ile
20 25 30

Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg
35 40 45

Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly
50 55 60

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Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly
 65 70 75 80
 Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile
 85 90 95
 Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His
 100 105 110
 Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg
 115 120 125
 Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu
 130 135 140
 Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val
 145 150 155 160
 Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe
 165 170 175
 Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu
 180 185 190
 Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val
 195 200 205
 Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu His Leu Cys Gly Ala
 210 215 220
 Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser
 225 230 235 240
 Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp
 245 250 255
 Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg
 260 265 270
 Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn
 275 280 285
 Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro
 290 295 300
 Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser
 305 310 315 320
 Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys
 325 330 335
 Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu
 340 345 350
 Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu
 355 360 365
 Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp
 370 375 380
 Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met
 385 390 395 400

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Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg
405 410 415

Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe
420 425 430

Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp
435 440 445

Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser
450 455

<210> 25

<211> 1302

<212> DNA

<213> Homo sapiens

<400> 25

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gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 180
gtgggcagcc ccccgccagac gctcaacatc ctggtggtata caggcagcag taactttgca 240
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gtgcacatca ctgaatcaga caagtttttc atcaacggct ccaactggga aggcatcctg 480
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gaccactcgc tgtacacagg cagtctctgg tatacaccca tccggcgggg gtggatttat 720
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catgtgcacg atgagttcag gacggcagcg gtggaaaggcc ctttgtcac cttggacatg 1260
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<210> 26

<211> 433

<212> PRT

<213> Homo sapiens

<400> 26

Met Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly
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Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu
20 25 30

Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg
35 40 45

Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro
50 55 60

Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala
65 70 75 80

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Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	His	Arg	Tyr	Tyr	Gln	Arg	Gln
									85	90					95
Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Ileu	Arg	Lys	Gly	Val	Tyr	Val	Pro	Tyr
									100	105					110
Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly	Thr	Asp	Leu	Val	Ser	Ile
									115	120					125
Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala	Asn	Ile	Ala	Ala	Ile	Thr
									130	135					140
Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser	Asn	Trp	Glu	Gly	Ile	Leu
									145	150					160
Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro	Asp	Asp	Ser	Leu	Glu	Pro
									165	170					175
Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His	Val	Pro	Asn	Leu	Phe	Ser
									180	185					190
Leu	His	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu	Asn	Gln	Ser	Glu	Val	Leu
									195	200					205
Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly	Gly	Ile	Asp	His	Ser	Leu
									210	215					220
Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile	Arg	Arg	Glu	Trp	Tyr	Tyr
									225	230					240
Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn	Gly	Gln	Asp	Leu	Lys	Met
									245	250					255
Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser	Ile	Val	Asp	Ser	Gly	Thr
									260	265					270
Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe	Glu	Ala	Ala	Val	Lys	Ser
									275	280					285
Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe	Pro	Asp	Gly	Phe	Trp	Leu
									290	295					300
Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly	Thr	Thr	Pro	Trp	Asn	Ile
									305	310					320
Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly	Glu	Val	Thr	Asn	Gln	Ser
									325	330					335
Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr	Leu	Arg	Pro	Val	Glu	Asp
									340	345					350
Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys	Phe	Ala	Ile	Ser	Gln	Ser
									355	360					365
Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile	Met	Glu	Gly	Phe	Tyr	Val
									370	375					380
Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	Gly	Phe	Ala	Val	Ser	Ala	Cys
									385	390					400
His	Val	His	Asp	Glu	Phe	Arg	Thr	Ala	Ala	Val	Glu	Gly	Pro	Phe	Val
									405	410					415

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Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu
420 425 430

Ser

<210> 27

<211> 1278

<212> DNA

<213> Homo sapiens

<400> 27

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ggcaagtccg	ggcaggggcta	ctacgtggag	atgaccgtgg	gcagcccccc	gcagacgctc	180
aacatccctgg	tggatacagg	cagcagtaac	tttgcagtgg	gtgtgtcccc	ccaccccttc	240
ctgcatcgct	actaccagag	gcagactgtcc	agcacatacc	gggacccctcg	gaagggtgtg	300
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ccccatggcc	ccaaacgtc	tgtgcgtgcc	aacattgtgg	ccatcaactga	atcagacaag	420
ttcttcatca	acggctccaa	ctgggaagg	atcctggggc	tggcctatgc	tgagattgcc	480
aggcctgacg	actccctgga	gcctttctt	gactctctgg	taaagcagac	ccacgttccc	540
aacctcttct	ccctgcac	ttgtggtgc	ggcttcccc	tcaaccagtc	tgaagtgtcg	600
gcctctgtcg	gagggagcat	gatcattgg	ggtatcgacc	actcgctgt	cacaggcagt	660
ctctggata	caccatccg	gcgggagtg	tattatgagg	tcatcattgt	gcgggtggag	720
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gtgtgtgtgc	aaggcaggc	cacccttgg	aacattttcc	cagtcatctc	actctaccta	960
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tccacggca	ctgttatgg	agctgttatac	atggagggt	tctacgttgt	ctttgatcg	1140
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gcagcgggtgg	aaggccctt	tgtcacctt	gacatggaa	actgtggcta	caacattcca	1260
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<210> 2B

<211> 425

<212> PRT

<213> Homo sapiens

<400> 28

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Met Thr
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Ile Ser Asp Ser Pro Leu Asp Ser Gly Ile Glu Thr Asp Gly Ser Phe
20 25 30

Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr
 35 40 45

Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val
50 55 60

Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	Pro	Phe
65					70				75						80

Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu
85 90 95

Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu
100 105 110

Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val
115 120 125

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Arg	Ala	Asn	Ile	Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn
130						135					140				
Gly	Ser	Asn	Trp	Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala
145						150				155			160		
Arg	Pro	Asp	Asp	Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln
	165						170					175			
Thr	His	Val	Pro	Asn	Leu	Phe	Ser	Leu	His	Leu	Cys	Gly	Ala	Gly	Phe
	180						185				190				
Pro	Leu	Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	Ser	Met	Ile
	195						200				205				
Ile	Gly	Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr
210						215				220					
Pro	Ile	Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu
225						230				235			240		
Ile	Asn	Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp
	245						250				255				
Lys	Ser	Ile	Val	Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys
	260						265				270				
Val	Phe	Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu
	275					280				285					
Lys	Phe	Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln
	290						295				300				
Ala	Gly	Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu
305							310				315			320	
Met	Gly	Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln
	325							330				335			
Gln	Tyr	Leu	Arg	Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys
	340							345				350			
Tyr	Lys	Phe	Ala	Ile	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val	Met	Gly	Ala
	355							360				365			
Val	Ile	Met	Glu	Gly	Phe	Tyr	Val	Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg
	370						375				380				
Ile	Gly	Phe	Ala	Val	Ser	Ala	Cys	His	Val	His	Asp	Glu	Phe	Arg	Thr
385							390				395			400	
Ala	Ala	Val	Glu	Gly	Pro	Phe	Val	Thr	Leu	Asp	Met	Glu	Asp	Cys	Gly
	405							410				415			
Tyr	Asn	Ile	Pro	Gln	Thr	Asp	Glu	Ser							
	420						425								

<210> 29
<211> 1362
<212> DNA
<213> Homo sapiens

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<400> 29

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ctgcggctgc cccgggagac cgacgaagag cccqaggagc cggccggag gggcagctt 180
gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240
gtggcagcc ccccgagac gctcaacatc ctggtgata caggcagcag taactttgca 300
gtgggtctg cccccccaccc ctgcctgcat cgctactacc agaggcagct gtccagcaca 360
tacgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag 420
ctggccaccg acctggtaag catccccat ggccccaacg tcactgtcg tgccaaacatt 480
gctccatca ctgaatcaga caagtttcc atcaacggct ccaactggga aggcatcctg 540
gggctggctt atgctggat tgccaggctt gacgactccc tggagccctt ctttgcactt 600
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gaccactcgc tggacacagg cagtcttgg tatacacccca tccggcgga gtggatttat 780
gaggtcatca ttgtgcgggtt ggagatcaat ggacaggatc tgaaaaatgga ctgcaaggag 840
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gtgttgaag ctgcagtcaa atccatcaag gcacgcctt ccacggagaa gttccctgat 960
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ggcttctacg ttgtcttgc tccggcccgaa aaacgaattt gctttgtgtt cagcgcttgc 1260
catgtgcacg atgagttcag gacggcagcg gtggaaaggcc ctttgtcac cttggacatg 1320
gaagactgtg gctacaacat tccacagaca gatgagtcat ga 1362

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<210> 30

<211> 453

<212> PRT

<213> Homo sapiens

<400> 30

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1				5					10				15		

Leu	Pro	Ala	His	Gly	Thr	Gln	His	Gly	Ile	Arg	Leu	Pro	Leu	Arg	Ser
						20			25				30		

Gly	Leu	Gly	Gly	Ala	Pro	Leu	Gly	Leu	Arg	Leu	Pro	Arg	Glu	Thr	Asp
				35				40				45			

Glu	Glu	Pro	Glu	Glu	Pro	Gly	Arg	Arg	Gly	Ser	Phe	Val	Glu	Met	Val
					50			55			60				

Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val	Glu	Met	Thr
	65				70					75		80			

Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp	Thr	Gly	Ser
					85				90			95			

Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	His	Arg	Tyr
				100				105				110			

Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys	Gly	Val
					115			120			125				

Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly	Thr	Asp
					130			135			140				

Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala	Asn	Ile
					145			150			155			160	

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Ala Ala Ile Thr Glu Ser Asp Lys Phe	Phe Ile Asn Gly Ser Asn Trp		
165	170	175	
Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp			
180	185	190	
Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro			
195	200	205	
Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln			
210	215	220	
Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile			
225	230	235	240
Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg			
245	250	255	
Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln			
260	265	270	
Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val			
275	280	285	
Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala			
290	295	300	
Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp			
305	310	315	320
Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr			
325	330	335	
Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val			
340	345	350	
Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg			
355	360	365	
Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala			
370	375	380	
Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu			
385	390	395	400
Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala			
405	410	415	
Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu			
420	425	430	
Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro			
435	440	445	
Gln Thr Asp Glu Ser			
450			

<210> 31
<211> 1380
<212> DNA

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<213> Homo sapiens

<400> 31

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 ctgcggctgc cccgggagac cgacgaagag cccgaggagc cggccggag gggcagctt 180
 gtggagatgg tggacaacct gagggcaag tcggggcagg gctactacgt ggagatgacc 240
 gtggcagcc ccccgagac gtcacacate ctggggata caggcagcag taactttca 300
 gtgggtgctg ccccccaccc ttccctgcat cgctactacc agggcaggt gtccagcaca 360
 taccgggacc tcggaaaggc tggttatgtg ccctacacc agggcaagt ggaaggggag 420
 ctggcaccgc acctggtaa catccccat gcccccaacg tcacttgctg tgccaacatt 480
 gtcgcacatca ctgaatcaga caagtttcc atcaacggct ccaactggg aggcatcctg 540
 gggctggct atgctgagat tgccaggcct gacgactccc tggagcctt ctttactct 600
 ctggtaaaggc agacccacgt tcccaacctc ttctccctgc acctttgtgg tgctggctc 660
 cccctcaacc agtctgaatg gctggcctc gtccggaggg gcatgatcat tggaggtatc 720
 gaccactcgc tgcacacagg cagtctctgg tatacacca tccggcggg gtggattat 780
 gaggtcatca ttgtgcgggt ggagatcaat ggacaggatc taaaatggg ctgcaaggag 840
 tacaactatg acaagagcat tggtggacagt ggcaccacca accttcgtt gccaagaaaa 900
 gtgtttaagg ctgcagtcaa atccatcaag gcaacctct ccacggagaa gttccctgtat 960
 ggtttctggc taggagagca gctgggtgtc tggcaagcag gcaaccaccc ttggAACATT 1020
 ttcccagtca ttcactcta cctaattggg gaggttacca accagtctt ccgcattacc 1080
 atcctccgc agcaataacct gcccggatc gaaatgtgg ccacgtccca agacgactgt 1140
 tacaatttg ccatctcaca gtcatccacg ggcactgtt tggagctgt tatcatggag 1200
 ggcttctacg ttgtcttga tcggggccgaa aacgaattt gctttgtctg cagcgttgc 1260
 catgtgcacg atgagtttag gacggcagcg gtggaaaggcc ctttgtcac tttggacatg 1320
 gaagactgtg gtcacacat tccacagaca gatggatcagc agcagcagca gcagcagtga 1380

<210> 32

<211> 459

<212> PRT

<213> Homo sapiens

<400> 32

Met	Ala	Gln	Ala	Leu	Pro	Trp	Leu	Leu	Leu	Trp	Met	Gly	Ala	Gly	Val
1				5				10					15		

Leu	Pro	Ala	His	Gly	Thr	Gln	His	Gly	Ile	Arg	Leu	Pro	Leu	Arg	Ser
					20			25					30		

Gly	Leu	Gly	Gly	Ala	Pro	Leu	Gly	Leu	Arg	Leu	Pro	Arg	Glu	Thr	Asp
					35			40				45			

Glu	Glu	Pro	Glu	Glu	Pro	Gly	Arg	Arg	Gly	Ser	Phe	Val	Glu	Met	Val
					50			55			60				

Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val	Glu	Met	Thr
					65			70		75		80			

Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp	Thr	Gly	Ser
					85			90			95				

Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	His	Arg	Tyr
					100			105			110				

Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys	Gly	Val
					115			120			125				

Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly	Thr	Asp
					130			135			140				

Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala	Asn	Ile
					145			150		155		160			

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Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
180 185 190

Ser Leu Glu Pro Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
195 200 205

Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
210 215 220

Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
225 230 235 240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
245 250 255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
260 265 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
275 280 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
370 375 380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
405 410 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
420 425 430

Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
435 440 445

Gln Thr Asp Glu Ser His His His His His His His
450 455

<210> 33
<211> 25

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<212> PRT
<213> Homo sapiens

<400> 33
Ser Glu Gln Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu
1 5 10 15

Ser Ser Leu Val Arg His Arg Trp Lys
20 25

<210> 34
<211> 19
<212> PRT
<213> Homo sapiens

<400> 34
Ser Glu Gln Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp Ile Ser
1 5 10 15

Leu Leu Lys

<210> 35
<211> 29
<212> DNA
<213> Homo sapiens

<400> 35
gtggatccac ccagcacggc atccggctg 29

<210> 36
<211> 36
<212> DNA
<213> Homo sapiens

<400> 36
gaaagctttc atgactcatc tgtctgtgga atgttg 36

<210> 37
<211> 39
<212> DNA
<213> Homo sapiens

<400> 37
gatcgatgac tatctctgac tctccgcgtg aacaggacg 39

<210> 38
<211> 39
<212> DNA
<213> Homo sapiens

<400> 38
gatccgtcct gttcacgcgg agagtcagag atagtcattc 39

<210> 39
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hu-Asp2

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<400> 39
cggcatccgg ctgcccctgc gtagcggtct gggtggtgct ccactgggtc tgcgtctgcc 60
ccgggagacc gacgaag 77

<210> 40
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hu-Asp2

<400> 40
cttcgtcggt ctccccggggc agacgcagac ccagtggagc accacccaga ccgctacgca 60
ggggcagccg gatgccg 77

<210> 41
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase 8
Cleavage Site

<400> 41
gatcgatgac tatctctgac tctccgctgg actctggtat cgaaaccgac g 51

<210> 42
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase 8
Cleavage Site

<400> 42
gatccgtcgg ttccgatacc agagtccagc ggagagtcag agatagtcat c 51

<210> 43
<211> 32
<212> DNA
<213> Homo sapiens

<400> 43
aaggatcatt tgtggagatg gtggacaacc tg 32

<210> 44
<211> 36
<212> DNA
<213> Homo sapiens

<400> 44
gaaagcttcc atgactcatc tgtctgtgga atgttg 36

<210> 45
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 6-His tag

47
ccac tcgaccagggt tc

22

48
51
DNA
Artificial Sequence

Description of Artificial Sequence: primer

48
aaat tccagcacac tggctacttc ttgttctgca tctcaaagaa c 51

49
26
DNA
Artificial Sequence

Description of Artificial Sequence: primer

49
taaat tccagcacac tggcta 26

50
1287
DNA
Artificial Sequence

Description of Artificial Sequence: Hu-Asp2(b)
delta TM

50
ccaag ccctgccctg gtcctgtctg tggatggcg cgggagtgct gcctgcccac 60
ccagc acggcatccg gctgccctg cgacgcggcc tggggggcgcc cccccctgggg 120
gtgc cccggagac cgacgaagag cccgaggagc ccggccggag gggcagctt 180
gatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240
cagcc ccccgagac gctcaacatc ctggtgata caggcagcag taacttgca 300
tgctg ccccccaccc cttcctgcat cgctactacc agaggcagct gtccagcaca 360

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PCT/IB01/00797

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45
atca tcaccatcac catg

24

46
24
DNA
Artificial Sequence

Description of Artificial Sequence: 6-His tag

46
tgtt gatgggtatg atgc 24

47
22
DNA
Artificial Sequence

Description of Artificial Sequence: primer

- 43 -

taccgggacc tccggaaggg ttgttatgtc ccctacaccc agggcaagtg ggaaggggag 420
 ctgggcaccc acctggtaag catccccat ggccccaaacg tcactgtcg tgccaacatt 480
 gctccatca ctgaatcaga caagttcttc atcaacgct ccaactggg aggcatccg 540
 gggctggct atgctgagat tgccaggctt tgggtgtcg gcttccccc caaccagtct 600
 gaagtgtgg cctctgtcg aggagcatg atcattggag gtatcgacca ctcgctgtac 660
 acaggcagtc tctggatac acccatccg cgggagtggt attatgaggt catcattgtg 720
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 agcattgtgg acagtggcac caccaccc ttgactgcca agaaagtgtt tgaagctgca 840
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 gagcagctgg tggctggca agcaggcacc acccccttgg acatttccc agtcatctca 960
 ctctaccta tgggtgaggt tccaaccag tccttccgca tcaccatctt tccgcagcaa 1020
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 tcacagtcat ccacgggcac tggatggaa gctgttatca tggagggctt ctacgttgc 1140
 tttgatcgccc cccgaaacg aattggctt gctgtcagcg cttgccatgt gcacgatgag 1200
 ttcaggacgg cagcggtgga aggcctttt gtcaccttgg acatggaga ctgtggctac 1260
 aacattccac agacagatga gtcatga 1287

<210> 51

<211> 428

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hu-Asp2(b)
 delta TM

<400> 51

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
 1 5 10 15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
 20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
 35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
 50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
 65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
 85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
 100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
 115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
 130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
 145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
 165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Leu Cys Gly
 180 185 190

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Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly
 195 200 205
 Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu
 210 215 220
 Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val
 225 230 235 240
 Arg Val Glu Ile Asn Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr
 245 250 255
 Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu
 260 265 270
 Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser
 275 280 285
 Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val
 290 295 300
 Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser
 305 310 315 320
 Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile
 325 330 335
 Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln
 340 345 350
 Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val
 355 360 365
 Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala
 370 375 380
 Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu
 385 390 395 400
 Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu
 405 410 415
 Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser
 420 425

<210> 52
 <211> 1305
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Hu-Asp2(b)
 delta TM

<400> 52
 atggcccaag ccctgcctcg gctcctgctg tggatggcg cgggagtgt gcctgccac 60
 ggcaccggc acggcatccg gctgccccctg cgcaaggccc tggggggcgc cccctgggg 120
 ctgcggctgc cccgggagac cgacgaagag cccgaggagc cccggccggag gggcagctt 180
 gtggagatgg tgacaacctt gaggggcaag tcggggcagg gctactacgt ggagatgacc 240
 gtggcagcc ccccgagac gctcaacatc ctggtgata caggcagcag taacttgca 300
 gtgggtgctg ccccccaccc ctccctgcat cgctactacc agaggcagct gtccagcaca 360
 taccggacc tccggaaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaagggag 420

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ctgggcacccg acctggtaag catccccat ggccccaacg tcactgtcg cgccaaacatt 480
gctgccatca ctgaatcaga caaggcttc atcaacggct ccaactggga aggcatctg 540
gggctggct atgctgagat tgccaggctt tgtggtgctg gcttccccct caaccagtct 600
gaagtgtctgg cctctgtcgg agggagcatg atcattggag gtatcgacca ctcgctgtac 660
acaggcagtc tctggtatac acccatccgg cgggagtggtt attatgaggt catcatgtg 720
cgggtggaga tcaatggaca ggatctgaaa atggactgca aggagtacaa ctatgacaag 780
agcattgtgg acagtggcac caccAACCTT cgTTTGGCCA agaaagtgtt tgaagctgca 840
gtcaaatcca tcaaggcagc ctccTCCACG gagaagttcc ctgtatggttt ctggcttagg 900
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<210> 53

<211> 434

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hu-Asp2(b)
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<400> 53

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Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
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Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
 130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Leu Cys Gly
 180 185 190

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Ala	Gly	Phe	Pro	Leu	Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly
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Ser	Met	Ile	Ile	Gly	Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu
210						215				220					
Trp	Tyr	Thr	Pro	Ile	Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val
225					230			235			240				
Arg	Val	Glu	Ile	Asn	Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr
	245						250		255						
Asn	Tyr	Asp	Lys	Ser	Ile	Val	Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu
					260			265				270			
Pro	Lys	Lys	Val	Phe	Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser
					275			280			285				
Ser	Thr	Glu	Lys	Phe	Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val
					290			295			300				
Cys	Trp	Gln	Ala	Gly	Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser
					305			310		315			320		
Leu	Tyr	Leu	Met	Gly	Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile
					325				330			335			
Leu	Pro	Gln	Gln	Tyr	Leu	Arg	Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln
					340			345			350				
Asp	Asp	Cys	Tyr	Lys	Phe	Ala	Ile	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val
					355			360			365				
Met	Gly	Ala	Val	Ile	Met	Glu	Gly	Phe	Tyr	Val	Val	Phe	Asp	Arg	Ala
					370			375			380				
Arg	Lys	Arg	Ile	Gly	Phe	Ala	Val	Ser	Ala	Cys	His	Val	His	Asp	Glu
					385			390		395			400		
Phe	Arg	Thr	Ala	Ala	Val	Glu	Gly	Pro	Phe	Val	Thr	Leu	Asp	Met	Glu
					405				410			415			
Asp	Cys	Gly	Tyr	Asn	Ile	Pro	Gln	Thr	Asp	Glu	Ser	His	His	His	His
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His His															

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<211> 2310
<212> DNA
<213> Homo sapiens

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ctgaacatgc acatgaatgt ccagaatggg aagtggatt cagatccatc agggaccaaa 180
acctgcattt ataccaagga aggcatctg cagtattgcc aagaagtcta ccctgaactg 240
cagatcacca atgtggtaga agccaaccaa ccagtgacca tccagaactg gtgcaagcgg 300
ggccgcaagc agtgcaagac ccatccccac tttgtgattc cttaccgctg cttagtttgt 360

- 47 -

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aagagtacca	acttgcata	ctacggcatg	ttgctgcctt	gcggatttg	caagttccga	540
ggggtagagt	ttgtgtgtt	cccactggct	gaagaaaatg	acaatgtgg	ttctgtgtat	600
gcggaggagg	atgactcgga	tgtctgggt	ggcggagcag	atacagacta	tgcagatggg	660
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gagtctgtgg	aagagggtgt	tcgagaggt	tgctctgaac	aagccgagac	ggggccgtgc	900
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gctgtcaccc	cagaggagcg	ccacctgtcc	aagatgcagc	agaacggcta	cgaaaatccs	2280
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<210> 55

<211> 770

<212> PRT

<213> Homo sapiens

<400> 55

Met Leu P

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Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu

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20 25 30

20 20 30

Gln Ile Asn Met Phe Cys Gly Arg Leu Asp Met His Met Asp Val

Gln Thr Ala Met Phe Cys Gly Arg Leu Asn Met His Lys Met Asn Val
35 18 45

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Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile

50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
85 90 95

Trp Cys Lys Arg Gly Arg Lys Cln Cys Lys Thr His Pro His Phe Val
 100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125

- 48 -

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys		
130	135	140
Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu		
145	150	155
160		
Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile		
165	170	175
Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu		
180	185	190
Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val		
195	200	205
Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys		
210	215	220
Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu		
225	230	235
240		
Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu		
245	250	255
Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile		
260	265	270
Ala Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg		
275	280	285
Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile		
290	295	300
Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe		
305	310	315
320		
Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr		
325	330	335
Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr		
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Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala		
355	360	365
Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp		
370	375	380
Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala		
385	390	395
400		
Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala		
405	410	415
Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile		
420	425	430
Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn		
435	440	445
Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met		
450	455	460

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Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu
465 470 475 480

Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys
485 490 495

Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe
500 505 510

Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser
515 520 525

Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser
530 535 540

Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp
545 550 555 560

Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val
565 570 575

Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala
580 585 590

Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Val Glu Leu Leu Pro
595 600 605

Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe
610 615 620

Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val
625 630 635 640

Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser
645 650 655

Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp
660 665 670

Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu
675 680 685

Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly
690 695 700

Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu
705 710 715 720

Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val
725 730 735

Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met
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Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met
755 760 765

Gln Asn
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<210> 56
<211> 2253
<212> DNA
<213> Homo sapiens

<400> 56
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acctgcattt atacaaggaa aggcatctg cagatttgc aagaagtcta ccctgaactg 240
cagatccacca atgtgttaga agccaaccac ccagtgcacca tccagaactg gtgcaagcgg 300
ggccgcaagc aytgcagac ccatccccac ttgtgttcc cttaccgcgtc cttagtttgt 360
gagttgttaa gtgtgtccct tctcggttcc gacaagtgc aatttcttaca ccaggagagg 420
atggatgttt gcaaactca tcttcactgg cacaccgtcg ccaaaagagac atgcagttag 480
aagagtacca acttgcattga ctacggcatg ttgtgtccct gcgaaattga caagttccga 540
ggggtagagt ttgtgttgtt cccactggct gaagaaagtg acaatgttgc ttctgctgt 600
gcggaggagg atgactcgga tgtctgttgg ggcggagcag acacagacta tgcatgtggg 660
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gaagccgatg atgacgagggat cgatgaggat ggtgtgtgg tagaggaaga ggctgaggaa 780
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<212> PRT
<213> Homo sapiens

<400> 57
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20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
50 55 60

- 51 -

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
 65 70 75 80
 Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
 85 90 95
 Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
 100 105 110
 Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
 115 120 125
 Val Pro Asp Lys Cys Lys Phe Leu His Cln Glu Arg Met Asp Val Cys
 130 135 140
 Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
 145 150 155 160
 Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
 165 170 175
 Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
 180 185 190
 Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Asp Asp Ser Asp Val
 195 200 205
 Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
 210 215 220
 Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
 225 230 235 240
 Glu Ala Asp Asp Asp Glu Asp Asp Gly Asp Glu Val Glu Glu
 245 250 255
 Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
 260 265 270
 Ala Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Val Val Arg
 275 280 285
 Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
 290 295 300
 Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
 305 310 315 320
 Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
 325 330 335
 Cys Met Ala Val Cys Gly Ser Ala Ile Pro Thr Thr Ala Ala Ser Thr
 340 345 350
 Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp Glu Asn Glu
 355 360 365
 His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala Lys His Arg
 370 375 380
 Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala Glu Arg Gln
 385 390 395 400

- 52 -

Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile Gln His Phe
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 Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn Glu Arg Gln
 420 425 430
 Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met Leu Asn Asp
 435 440 445
 Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu Gln Ala Val
 450 455 460
 Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys Tyr Val Arg
 465 470 475 480
 Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe Glu His Val
 485 490 495
 Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser Gln Val Met
 500 505 510
 Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser Leu Ser Leu
 515 520 525
 Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp Glu Val Asp
 530 535 540
 Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val Leu Ala Asn
 545 550 555 560
 Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala Leu Met Pro
 565 570 575
 Ser Leu Thr Glu Thr Lys Thr Val Glu Leu Leu Pro Val Asn Gly
 580 585 590
 Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe Gly Ala Asp
 595 600 605
 Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val Asp Ala Arg
 610 615 620
 Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr
 625 630 635 640
 Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe
 645 650 655
 Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe
 660 665 670
 Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val
 675 680 685
 Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu Val Met Leu
 690 695 700
 Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val Glu Val Asp
 705 710 715 720
 Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met Gln Gln Asn
 725 730 735

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Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met Glu Asn
 740 745 750

<210> 58
<211> 2316
<212> DNA
<213> Homo sapiens

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cagatcacca atgtggtaga agccaaccaa ccagtggacca tccagaactg gtgcaagcgg 300
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cgagcaatgtt tctcccgctt gtactttgtt gtgactgttgc ggaagtgtgc cccattttt 960
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aagaaagccg ctccatgtt gtcggatgtt atgcacaccc tccgtgtgtt ttatgagcgc 1620
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aaaaccaccc tggagcttcc tccctgttcaat gggaggttca gcctggacca tctccagccg 1860
tggcattttt tttggggcttca ctctgtgcac ccacccacag aaaaccaatgt tgagcctgtt 1920
gatgcggccctt ctgtgcgcgc ccggggactt accactcgac cagggttctgg gttgacaaat 1980
atcaagacccgg aggatgttca tggatgttcaat gggggatgttca tggatgttca 2040
tatgaatgttca atcaataaaaa atttttttt ttttttttcaat gggggatgttca aacaaatgtt 2100
gcaatcatgtt gactcatgtt gggcggtttt gtcatagcgtt cagttgtatgtt catcaccctt 2160
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<210> 59
<211> 772
<212> PRT
<213> Homo sapiens

<400> 59
Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg
 1 5 10 15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
 20 25 30

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Gln	Ile	Ala	Met	Phe	Cys	Gly	Arg	Leu	Asn	Met	His	Met	Asn	Val	Gln
35								40						45	
Asn	Gly	Lys	Trp	Asp	Ser	Asp	Pro	Ser	Gly	Thr	Lys	Thr	Cys	Ile	Asp
	50						55				60				
Thr	Lys	Glu	Gly	Ile	Leu	Gln	Tyr	Cys	Gln	Glu	Val	Tyr	Pro	Glu	Leu
	65				70				75				80		
Gln	Ile	Thr	Asn	Val	Val	Glu	Ala	Asn	Gln	Pro	Val	Thr	Ile	Gln	Asn
		85						90					95		
Trp	Cys	Lys	Arg	Gly	Arg	Lys	Gln	Cys	Lys	Thr	His	Pro	His	Phe	Val
		100					105				110				
Ile	Pro	Tyr	Arg	Cys	Leu	Val	Gly	Glu	Phe	Val	Ser	Asp	Ala	Leu	Leu
	115					120					125				
Val	Pro	Asp	Lys	Cys	Lys	Phe	Leu	His	Gln	Glu	Arg	Met	Asp	Val	Cys
	130					135				140					
Glu	Thr	His	Leu	His	Trp	His	Thr	Val	Ala	Lys	Glu	Thr	Cys	Ser	Glu
	145					150				155			160		
Lys	Ser	Thr	Asn	Leu	His	Asp	Tyr	Gly	Met	Leu	Leu	Pro	Cys	Gly	Ile
		165					170					175			
Asp	Lys	Phe	Arg	Gly	Val	Glu	Phe	Val	Cys	Cys	Pro	Leu	Ala	Glu	Glu
		180				185						190			
Ser	Asp	Asn	Val	Asp	Ser	Ala	Asp	Ala	Glu	Glu	Asp	Asp	Ser	Asp	Val
		195				200					205				
Trp	Trp	Gly	Gly	Ala	Asp	Thr	Asp	Tyr	Ala	Asp	Gly	Ser	Glu	Asp	Lys
	210					215				220					
Val	Val	Glu	Val	Ala	Glu	Glu	Glu	Val	Ala	Glu	Val	Glu	Glu		
	225				230				235			240			
Glu	Ala	Asp	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Gly	Asp	Glu	Val	Glu	Glu
		245				250					255				
Glu	Ala	Glu	Glu	Pro	Tyr	Glu	Glu	Ala	Thr	Glu	Arg	Thr	Thr	Ser	Ile
		260				265				270					
Ala	Thr	Thr	Thr	Thr	Thr	Thr	Glu	Ser	Val	Glu	Glu	Val	Val	Arg	
		275				280				285					
Glu	Val	Cys	Ser	Glu	Gln	Ala	Glu	Thr	Gly	Pro	Cys	Arg	Ala	Met	Ile
		290				295				300					
Ser	Arg	Trp	Tyr	Phe	Asp	Val	Thr	Glu	Gly	Lys	Cys	Ala	Pro	Phe	Phe
	305				310				315				320		
Tyr	Gly	Gly	Cys	Gly	Gly	Asn	Arg	Asn	Asn	Phe	Asp	Thr	Glu	Glu	Tyr
		325					330				335				
Cys	Met	Ala	Val	Cys	Gly	Ser	Ala	Met	Ser	Gln	Ser	Leu	Leu	Lys	Thr
		340					345				350				
Thr	Gln	Glu	Pro	Leu	Ala	Arg	Asp	Pro	Val	Lys	Leu	Pro	Thr	Thr	Ala
		355				360				365					

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Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp
 370 375 380
 Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala
 385 390 395 400
 Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala
 405 410 415
 Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile
 420 425 430
 Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn
 435 440 445
 Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met
 450 455 460

 Leu Asn Asp Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu
 465 470 475 480
 Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys
 485 490 495
 Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe
 500 505 510
 Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser
 515 520 525
 Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser
 530 535 540
 Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp
 545 550 555 560
 Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val
 565 570 575
 Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala
 580 585 590
 Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro
 595 600 605
 Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe
 610 615 620
 Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val
 625 630 635 640
 Asp Ala Arg Pro Ala Ala Asp Arg Gly Ile Thr Thr Arg Pro Gly Ser
 645 650 655
 Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp
 660 665 670
 Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu
 675 680 685
 Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly
 690 695 700

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Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu
 705 710 715 720
 Val Met Leu Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val
 725 730 735
 Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met
 740 745 750

Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met
 755 760 765

Gln Asn Lys Lys
770

<210> 60
<211> 2259
<212> DNA
<213> *Homo sapiens*

<400> 60
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ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaaa 180
acctgcattt ataccaagga aggcatccctg cagtattgcc aagaagtcta ccctgaactg 240
cagatcacca atggtgtttaga agccaaaccac ccagtgcacca tccagaactg gtgcgaagcgg 300
ggccgcgaagc agtgcacagac ccatccccac tttgtgattt cttaccyctg cttagttgt 360
gagttttaa gtgtatccct tctcgcttcc gacaatgtca aattcttaca ccaggagagg 420
atggatgttt gcgaaactt ctttcaacttgg caca:cgtcg ccaaagagac atgcagttag 480
aagagtacca atttgcattga ctacggcatg ttgtgtccct ggccaatttga caagttccga 540
ggggtagagt ttgtgtgttg cccactggtt gaaagaaagtg acaatgttgg ttctgtgtat 600
gcggaggagg atgactcgga tgtctgggtt ggccggagcag acacagacta tgccatgtgg 660
agtgaagaca aagttagtata agtagcagag gaggaaagaag tggctgaggt ggaagaagaa 720
gaagccgatg atgacgagga cgatgaggat ggtgtatggg tagaggaaga ggctgaggaa 780
ccctacgaag aagccacaga gagaaccacc agcattgcca ccaccaccac caccaccaca 840
gagtctgtgg aagagggtgt tcgagaggtt tgctctgaac aagccgagac gggccgtgc 900
cgagcaatga tctcccgctg gtacttttatgtt gtgactgaag ggaagtgtgc cccattttt 960
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tgtggcagcg ccatttcctac aacagcagcc agtacccctg atggccgttg caagatctc 1080
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ggatgtatgg ttcatcatca aaaattgggt ttcttgcag aagatgtggg ttcaaaacaaa 2040
ggtgcataca ttggactcat ggtggggcgt gttgtcatag cgacagtgtat cgtcatcacc 2100
ttgggtatgc tgaagaagaa acagttacaca tccatcatc atgggtgtgtt ggaggttgac 2160
gcccgtgtca ccccaagagga ggcgcacccctg tccaaatgtc agcagaacccg ctacgaaaat 2220
ccaaacctaca agtttttgcgacatgc aacaaaggaa 2259

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<210> 61

<211> 753

<212> PRT

<213> Homo sapiens

<400> 61

Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg
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Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210 215 220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
260 265 270

Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Val Arg
275 280 285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
290 295 300

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Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
 305 310 315 320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
 325 330 335

Cys Met Ala Val Cys Gly Ser Ala Ile Pro Thr Thr Ala Ala Ser Thr
 340 345 350

Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp Glu Asn Glu
 355 360 365

His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala Lys His Arg
 370 375 380

Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala Glu Arg Gln
 385 390 395 400

Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile Gln His Phe
 405 410 415

Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn Glu Arg Gln
 420 425 430

Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met Leu Asn Asp
 435 440 445

Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu Gln Ala Val
 450 455 460

Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys Tyr Val Arg
 465 470 475 480

Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe Glu His Val
 485 490 495

Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser Gln Val Met
 500 505 510

Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser Leu Ser Leu
 515 520 525

Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp Glu Val Asp
 530 535 540

Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val Leu Ala Asn
 545 550 555 560

Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala Leu Met Pro
 565 570 575

Ser Leu Thr Glu Thr Lys Thr Val Glu Leu Leu Pro Val Asn Gly
 580 585 590

Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe Gly Ala Asp
 595 600 605

Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val Asp Ala Arg
 610 615 620

Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr
 625 630 635 640

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Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe
645 650 655

Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe
660 665 670

Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val
675 680 685

Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu Val Met Leu
690 695 700

Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val Glu Val Asp
705 710 715 720

Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met Gln Gln Asn
725 730 735

Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met Gln Asn Lys
740 745 750

Lys

<210> 62
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic

<400> 62
Leu Glu Val Leu Phe Gln Gly Pro
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<210> 63
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic

<400> 63

Ser Glu Val Asn Leu Asp Ala Glu Phe Arg
1 5 10

<210> 64
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic

<400> 64
Ser Glu Val Lys Met Asp Ala Glu Phe Arg
1 5 10

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<210> 65
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic

<400> 65
Arg Arg Gly Gly Val Val Ile Ala Thr Val Ile Val Gly Glu Arg
1 5 10 15

<210> 66
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 66
Asn Leu Asp Ala
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<210> 67
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 67
Glu Val Lys Met Asp Ala Glu Phe
1 5

<210> 68
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 68
Gly Arg Arg Gly Ser
1 5

<210> 69
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 69

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Thr Gln His Gly Ile Arg
1 5

<210> 70
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 70

Glu Thr Asp Glu Glu Pro
1 5

<210> 71
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 71
Met Cys Ala Glu Val Lys Met Asp Ala Glu Phe Lys Asp Asn Pro
1 5 10 15

<210> 72
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic

<400> 72

Asp Ala Glu Phe Arg
1 5

<210> 73
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic

<400> 73

Ser Glu Val Asn Leu
1 5